

SEQUENCE LISTING

<110> BASF Aktiengesellschaft
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<213> Corynebacterium diphtheriae
<220>
<221> CDS
<222> (1)..(1101)
<223> RDI00386

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tac acc gaa gcc gga gcg acg ctt cac gac gta acc atc gcc tac caa 96
Tyr Thr Glu Ala Gly Ala Thr Leu His Asp Val Thr Ile Ala Tyr Gln
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gca tgg ggc cac tac acc ggc acc aat ctc atc gtt ctc gaa cat gcc 144
Ala Trp Gly His Tyr Thr Gly Thr Asn Leu Ile Val Leu Glu His Ala
35 40 45
ctg acc ggc gac tct aac gct att tca tgg tgg gac gga ctg att ggc 192
Leu Thr Gly Asp Ser Asn Ala Ile Ser Trp Trp Asp Gly Leu Ile Gly
50 55 60
cct ggc aaa gca ctc gac acc aac cgc tac tgc atc cta tgc acc aac 240
Pro Gly Lys Ala Leu Asp Thr Asn Arg Tyr Cys Ile Leu Cys Thr Asn
65 70 75 80
gtg ctc gga gga tgc aaa gga tcc acc gga ccg agc agt cca cac cca 288
Val Leu Gly Gly Cys Lys Gly Ser Thr Gly Pro Ser Ser Pro His Pro
85 90 95
gac gga aaa cca tgg gga tcc aga ttt cca gcc ctt tca atc cgt gac 336
Asp Gly Lys Pro Trp Gly Ser Arg Phe Pro Ala Leu Ser Ile Arg Asp
100 105 110
ctt gtc aat gcc gaa aaa caa ctt ttc gac cac ctc ggc atc aat aaa 384
Leu Val Asn Ala Glu Lys Gln Leu Phe Asp His Leu Gly Ile Asn Lys
115 120 125
att cac gca atc atc ggc gga tcc atg gga ggc gca cgc acc ctc gaa 432
Ile His Ala Ile Ile Gly Gly Ser Met Gly Gly Ala Arg Thr Leu Glu
130 135 140
tgg gct gca ctc cac cca cac atg atg acg act gga ttc gtc ata gca 480
Trp Ala Ala Leu His Pro His Met Met Thr Thr Gly Phe Val Ile Ala
145 150 155 160
gtc tca gca cgc gca agc gct tgg caa atc ggt att caa act gca caa 528
Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Thr Ala Gln

	165	170	175	
atc agc gcc ata gaa ctc gac ccc cac tgg aac ggc ggc gat tac tac				576
Ile Ser Ala Ile Glu Leu Asp Pro His Trp Asn Gly Gly Asp Tyr Tyr	180	185	190	
agc ggt cac gca cca tgg gaa gga atc gcc gcc gct cgc cgg atc gcc				624
Ser Gly His Ala Pro Trp Glu Gly Ile Ala Ala Ala Arg Arg Ile Ala	195	200	205	
cac ctc acc tat cgc ggc gaa cta gaa ata gac gaa cga ttc ggc act				672
His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg Phe Gly Thr	210	215	220	
tcc gca caa cac ggt gaa aac cca ctc ggc ccc ttc cga gat cca cat				720
Ser Ala Gln His Gly Glu Asn Pro Leu Gly Pro Phe Arg Asp Pro His	225	230	235	240
caa cgt ttt gcg gtc acg agc tac ctc caa cac caa ggc atc aaa ctc				768
Gln Arg Phe Ala Val Thr Ser Tyr Leu Gln His Gln Gly Ile Lys Leu	245	250	255	
gct caa cga ttc gat gca ggt agt tac gtc gtg ctt acc gaa gcc ctc				816
Ala Gln Arg Phe Asp Ala Gly Ser Tyr Val Val Leu Thr Glu Ala Leu	260	265	270	
aat cgt cat gac atc gga cgc ggc cga ggc gga ctc aac aaa gcc ctc				864
Asn Arg His Asp Ile Gly Arg Gly Arg Gly Gly Leu Asn Lys Ala Leu	275	280	285	
agc gca atc aca gtc ccc atc atg att gct ggc gtt gat acc gat att				912
Ser Ala Ile Thr Val Pro Ile Met Ile Ala Gly Val Asp Thr Asp Ile	290	295	300	
ctc tac ccc tat cac cag caa gaa cac cta tca cga aat cta ggc aac				960
Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn Leu Gly Asn	305	310	315	320
cta ctc gct atg gca aaa atc agc tca cca gta ggc cac gac gct ttc				1008
Leu Leu Ala Met Ala Lys Ile Ser Ser Pro Val Gly His Asp Ala Phe	325	330	335	
ctc aca gaa ttc cga caa atg gag cga atc cta aga cat ttc atg gag				1056
Leu Thr Glu Phe Arg Gln Met Glu Arg Ile Leu Arg His Phe Met Glu	340	345	350	
ctt tcg gaa gga atc gac gat tcc ttc cga acc aaa cta gag cgc				1101
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tga				1104

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 <213> Corynebacterium diptheriae

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 35 40 45

Leu Thr Gly Asp Ser Asn Ala Ile Ser Trp Trp Asp Gly Leu Ile Gly
 50 55 60
 Pro Gly Lys Ala Leu Asp Thr Asn Arg Tyr Cys Ile Leu Cys Thr Asn
 65 70 75 80
 Val Leu Gly Gly Cys Lys Gly Ser Thr Gly Pro Ser Ser Pro His Pro
 85 90 95
 Asp Gly Lys Pro Trp Gly Ser Arg Phe Pro Ala Leu Ser Ile Arg Asp
 100 105 110
 Leu Val Asn Ala Glu Lys Gln Leu Phe Asp His Leu Gly Ile Asn Lys
 115 120 125
 Ile His Ala Ile Ile Gly Gly Ser Met Gly Gly Ala Arg Thr Leu Glu
 130 135 140
 Trp Ala Ala Leu His Pro His Met Met Thr Thr Gly Phe Val Ile Ala
 145 150 155 160
 Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Thr Ala Gln
 165 170 175
 Ile Ser Ala Ile Glu Leu Asp Pro His Trp Asn Gly Gly Asp Tyr Tyr
 180 185 190
 Ser Gly His Ala Pro Trp Glu Gly Ile Ala Ala Ala Arg Arg Ile Ala
 195 200 205
 His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg Phe Gly Thr
 210 215 220
 Ser Ala Gln His Gly Glu Asn Pro Leu Gly Pro Phe Arg Asp Pro His
 225 230 235 240
 Gln Arg Phe Ala Val Thr Ser Tyr Leu Gln His Gln Gly Ile Lys Leu
 245 250 255
 Ala Gln Arg Phe Asp Ala Gly Ser Tyr Val Val Leu Thr Glu Ala Leu
 260 265 270
 Asn Arg His Asp Ile Gly Arg Gly Arg Gly Gly Leu Asn Lys Ala Leu
 275 280 285
 Ser Ala Ile Thr Val Pro Ile Met Ile Ala Gly Val Asp Thr Asp Ile
 290 295 300
 Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn Leu Gly Asn
 305 310 315 320
 Leu Leu Ala Met Ala Lys Ile Ser Ser Pro Val Gly His Asp Ala Phe
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<210> 3

<211> 1149

<212> DNA

<213> Mycobacterium leprae

<220>
 <221> CDS
 <222> (1)..(1146)
 <223> RML02951

<220>
 <221> unsure

<222> 224 .. 224
 <223> All occurrences of n indicate any nucleotide

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gtc	ggc	ttg	gtc	gac	atc	ggc	tca	ctt	acc	acc	gaa	agc	ggt	gcc	gtc	96
Val	Gly	Leu	Val	Asp	Ile	Gly	Ser	Leu	Thr	Thr	Glu	Ser	Gly	Ala	Val	
			20					25					30			
atc	gac	gat	gtc	tgc	atc	gcc	gtt	cag	cgc	tgg	ggg	gaa	ttg	tcg	ccc	144
Ile	Asp	Asp	Val	Cys	Ile	Ala	Val	Gln	Arg	Trp	Gly	Glu	Leu	Ser	Pro	
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acg	cga	gac	aac	gta	gtg	atg	gta	ctg	cat	gca	ctc	acc	ggt	gac	tcg	192
Thr	Arg	Asp	Asn	Val	Val	Met	Val	Leu	His	Ala	Leu	Thr	Gly	Asp	Ser	
	50					55					60					
cac	atc	acc	ggg	ccc	gcc	gga	ccg	gga	cat	cnc	aca	ccc	ggc	tgg	tgg	240
His	Ile	Thr	Gly	Pro	Ala	Gly	Pro	Gly	His	Xaa	Thr	Pro	Gly	Trp	Trp	
65					70				75					80		
gac	tgg	ata	gct	gga	ccg	ggt	gca	cca	atc	gac	acc	aac	cgc	tgg	tgc	288
Asp	Trp	Ile	Ala	Gly	Pro	Gly	Ala	Pro	Ile	Asp	Thr	Asn	Arg	Trp	Cys	
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gcg	ata	gcc	acc	aac	gtg	ctg	ggc	ggt	tgc	cgt	ggc	tcc	acc	ggc	cct	336
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Ser	Ser	Leu	Ala	Arg	Asp	Gly	Lys	Pro	Trp	Gly	Ser	Arg	Phe	Pro	Leu	
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Ile	Ser	Ile	Arg	Asp	Gln	Val	Glu	Ala	Asp	Ile	Ala	Ala	Leu	Ala	Ala	
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Ala	Arg	Ala	Leu	Glu	Trp	Ile	Ile	Gly	His	Pro	Asp	Gln	Val	Arg	Ala	
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ggg	ctg	ttg	ctg	gcg	gtc	ggt	gtg	cgc	gcc	acc	gcc	gac	cag	atc	ggc	576
Gly	Leu	Leu	Leu	Ala	Val	Gly	Val	Arg	Ala	Thr	Ala	Asp	Gln	Ile	Gly	
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acc	caa	acc	acc	caa	atc	gca	gcc	atc	aag	aca	gac	ccg	aac	tgg	caa	624
Thr	Gln	Thr	Thr	Gln	Ile	Ala	Ala	Ile	Lys	Thr	Asp	Pro	Asn	Trp	Gln	
		195					200					205				
ggc	ggt	gac	tac	tac	gag	aca	ggg	agg	gca	cca	gag	aac	ggc	ttg	aca	672
Gly	Gly	Asp	Tyr	Tyr	Glu	Thr	Gly	Arg	Ala	Pro	Glu	Asn	Gly	Leu	Thr	

210	215	220	
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ggc ggg cgt tac gca gtg cag agt tac cta gag cac cag ggt gac aag Gly Gly Arg Tyr Ala Val Gln Ser Tyr Leu Glu His Gln Gly Asp Lys 260 265 270			816
cta ttg gcc cgc ttt gac gca ggc agc tac gtg gtc ttg acc gaa acg Leu Leu Ala Arg Phe Asp Ala Gly Ser Tyr Val Val Leu Thr Glu Thr 275 280 285			864
ctg aac agc cac gac gtt ggc cgg ggc cgc gga ggg atc ggt aca gcg Leu Asn Ser His Asp Val Gly Arg Gly Arg Gly Gly Ile Gly Thr Ala 290 295 300			912
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cgg ctc tac cca ctg cgc ttg cag cag gag ctg gcc gag atg ctg ccg Arg Leu Tyr Pro Leu Arg Leu Gln Gln Glu Leu Ala Glu Met Leu Pro 325 330 335			1008
ggc tgc acc ggg ctg cag gtt gta gac tcc acc tac ggg cac gac ggc Gly Cys Thr Gly Leu Gln Val Val Asp Ser Thr Tyr Gly His Asp Gly 340 345 350			1056
ttc ctg gtg gaa tcc gag gcc gtc ggc aaa ttg atc cgt caa acc ctc Phe Leu Val Glu Ser Glu Ala Val Gly Lys Leu Ile Arg Gln Thr Leu 355 360 365			1104
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tga			1149

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 <211> 382
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 <213> Mycobacterium leprae

<220>
 <221> unsure
 <222> 75 .. 75
 <223> All occurrences of Xaa indicate any amino acid

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 35 40 45
 Thr Arg Asp Asn Val Val Met Val Leu His Ala Leu Thr Gly Asp Ser

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Asp	Trp	Ile	Ala	Gly 85	Pro	Gly	Ala	Pro	Ile 90	Asp	Thr	Asn	Arg	Trp 95	Cys
Ala	Ile	Ala	Thr 100	Asn	Val	Leu	Gly	Gly 105	Cys	Arg	Gly	Ser	Thr 110	Gly	Pro
Ser	Ser	Leu 115	Ala	Arg	Asp	Gly	Lys 120	Pro	Trp	Gly	Ser	Arg 125	Phe	Pro	Leu
Ile 130	Ser	Ile	Arg	Asp	Gln	Val 135	Glu	Ala	Asp	Ile	Ala 140	Ala	Leu	Ala	Ala
Met 145	Gly	Ile	Thr	Lys	Val 150	Ala	Ala	Val	Val	Gly 155	Gly	Ser	Met	Gly 160	Gly
Ala	Arg	Ala	Leu	Glu 165	Trp	Ile	Ile	Gly	His 170	Pro	Asp	Gln	Val	Arg 175	Ala
Gly	Leu	Leu	Leu 180	Ala	Val	Gly	Val	Arg 185	Ala	Thr	Ala	Asp	Gln 190	Ile	Gly
Thr	Gln	Thr 195	Thr	Gln	Ile	Ala 200	Ala	Ile	Lys	Thr	Asp	Pro 205	Asn	Trp	Gln
Gly	Gly 210	Asp	Tyr	Tyr	Glu	Thr 215	Gly	Arg	Ala	Pro	Glu 220	Asn	Gly	Leu	Thr
Ile 225	Ala	Arg	Arg	Phe	Ala 230	His	Leu	Thr	Tyr	Arg 235	Ser	Glu	Val	Glu 240	Leu
Asp	Thr	Arg	Phe	Ala 245	Asn	Asn	Asn	Gln	Gly 250	Asn	Glu	Asp	Pro 255	Ala	Thr
Gly	Gly	Arg 260	Tyr	Ala	Val	Gln	Ser	Tyr 265	Leu	Glu	His	Gln	Gly 270	Asp	Lys
Leu	Leu	Ala 275	Arg	Phe	Asp	Ala	Gly 280	Ser	Tyr	Val	Val	Leu 285	Thr	Glu	Thr
Leu	Asn 290	Ser	His	Asp	Val	Gly 295	Arg	Gly	Arg	Gly	Gly 300	Ile	Gly	Thr	Ala
Leu 305	Arg	Gly	Cys	Pro	Val 310	Pro	Val	Val	Val	Gly 315	Gly	Ile	Thr	Ser 320	Asp
Arg	Leu	Tyr	Pro	Leu 325	Arg	Leu	Gln	Gln	Glu 330	Leu	Ala	Glu	Met	Leu 335	Pro
Gly	Cys	Thr 340	Gly	Leu	Gln	Val	Val	Asp 345	Ser	Thr	Tyr	Gly	His 350	Asp	Gly
Phe	Leu 355	Val	Glu	Ser	Glu	Ala	Val 360	Gly	Lys	Leu	Ile	Arg	Gln 365	Thr	Leu
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<211> 1140

<212> DNA

<213> Mycobacterium tuberculosis

<220>
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 <222> (1)..(1137)
 <223> RMTB03565

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Ile Asp Asp Val Cys Ile Ala Val Gln Arg Trp Gly Lys Leu Ser Pro	
35 40 45	
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Ala Arg Asp Asn Val Val Val Leu His Ala Leu Thr Gly Asp Ser	
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cac atc act gga ccc gcc gga ccc ggc cac ccc acc ccc ggc tgg tgg	240
His Ile Thr Gly Pro Ala Gly Pro Gly His Pro Thr Pro Gly Trp Trp	
65 70 75 80	
gac ggg gtg gcc ggg ccg agt gcg ccg att gac acc acc cgc tgg tgc	288
Asp Gly Val Ala Gly Pro Ser Ala Pro Ile Asp Thr Thr Arg Trp Cys	
85 90 95	
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Ala Val Ala Thr Asn Val Leu Gly Gly Cys Arg Gly Ser Thr Gly Pro	
100 105 110	
agc tcg ctt gcc cgc gac gga aag cct tgg ggc tca aga ttt ccg ctg	384
Ser Ser Leu Ala Arg Asp Gly Lys Pro Trp Gly Ser Arg Phe Pro Leu	
115 120 125	
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Ile Ser Ile Arg Asp Gln Val Gln Ala Asp Val Ala Ala Leu Ala Ala	
130 135 140	
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145 150 155 160	
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Ala Arg Ala Leu Glu Trp Val Val Gly Tyr Pro Asp Arg Val Arg Ala	
165 170 175	
gga ttg ctg ctg gcg gtc ggt gcg cgt gcc acc gca gac cag atc ggc	576
Gly Leu Leu Leu Ala Val Gly Ala Arg Ala Thr Ala Asp Gln Ile Gly	
180 185 190	
acg cag aca acg caa atc gcg gcc atc aaa gcc gac ccg gac tgg cag	624
Thr Gln Thr Thr Gln Ile Ala Ala Ile Lys Ala Asp Pro Asp Trp Gln	
195 200 205	
agc ggc gac tac cac gag acg ggg agg gca cca gac gcc ggg ctg cga	672
Ser Gly Asp Tyr His Glu Thr Gly Arg Ala Pro Asp Ala Gly Leu Arg	
210 215 220	
ctc gcc cgc cgc ttc gcg cac ctc acc tac cgc ggc gag atc gag ctc	720
Leu Ala Arg Arg Phe Ala His Leu Thr Tyr Arg Gly Glu Ile Glu Leu	
225 230 235 240	

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 Asp Thr Arg Phe Ala Asn His Asn Gln Gly Asn Glu Asp Pro Thr Ala
 245 250 255

ggc ggg cgc tac gcg gtg caa agt tat ctg gaa cac caa gga gac aaa 816
 Gly Gly Arg Tyr Ala Val Gln Ser Tyr Leu Glu His Gln Gly Asp Lys
 260 265 270

ctg tta tcc cgg ttc gac gcc ggc agc tac gtg att ctc acc gag gcg 864
 Leu Leu Ser Arg Phe Asp Ala Gly Ser Tyr Val Ile Leu Thr Glu Ala
 275 280 285

ctc aac agc cac gac gtc ggc cgc ggc cgc ggc ggg gtc tcc gcg gct 912
 Leu Asn Ser His Asp Val Gly Arg Gly Arg Gly Gly Val Ser Ala Ala
 290 295 300

ctg cgc gcc tgc ccg gtg ccg gtg gtg gtg ggc ggc atc acc tcc gac 960
 Leu Arg Ala Cys Pro Val Pro Val Val Val Gly Gly Ile Thr Ser Asp
 305 310 315 320

cgg ctc tac ccg ctg cgc ctg cag cag gag ctg gcc gac ctg ctg ccg 1008
 Arg Leu Tyr Pro Leu Arg Leu Gln Gln Glu Leu Ala Asp Leu Leu Pro
 325 330 335

ggc tgc gcc ggg ctg cga gtc gtc gag tcg gtc tac gga cac gac ggc 1056
 Gly Cys Ala Gly Leu Arg Val Val Glu Ser Val Tyr Gly His Asp Gly
 340 345 350

ttc ctg gtg gaa acc gag gcc gtg ggc gaa ttg atc cgc cag aca ctg 1104
 Phe Leu Val Glu Thr Glu Ala Val Gly Glu Leu Ile Arg Gln Thr Leu
 355 360 365

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<210> 6
 <211> 379
 <212> PRT
 <213> Mycobacterium tuberculosis

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Ile Asp Asp Val Cys Ile Ala Val Gln Arg Trp Gly Lys Leu Ser Pro
 35 40 45

Ala Arg Asp Asn Val Val Val Val Leu His Ala Leu Thr Gly Asp Ser
 50 55 60

His Ile Thr Gly Pro Ala Gly Pro Gly His Pro Thr Pro Gly Trp Trp
 65 70 75 80

Asp Gly Val Ala Gly Pro Ser Ala Pro Ile Asp Thr Thr Arg Trp Cys
 85 90 95

Ala Val Ala Thr Asn Val Leu Gly Gly Cys Arg Gly Ser Thr Gly Pro
 100 105 110

Ser Ser Leu Ala Arg Asp Gly Lys Pro Trp Gly Ser Arg Phe Pro Leu

115					120					125					
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130						135					140				
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145					150					155				160	
Ala	Arg	Ala	Leu	Glu	Trp	Val	Val	Gly	Tyr	Pro	Asp	Arg	Val	Arg	Ala
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Gly	Leu	Leu	Leu	Ala	Val	Gly	Ala	Arg	Ala	Thr	Ala	Asp	Gln	Ile	Gly
			180					185					190		
Thr	Gln	Thr	Thr	Gln	Ile	Ala	Ala	Ile	Lys	Ala	Asp	Pro	Asp	Trp	Gln
	195					200						205			
Ser	Gly	Asp	Tyr	His	Glu	Thr	Gly	Arg	Ala	Pro	Asp	Ala	Gly	Leu	Arg
210						215					220				
Leu	Ala	Arg	Arg	Phe	Ala	His	Leu	Thr	Tyr	Arg	Gly	Glu	Ile	Glu	Leu
225					230					235					240
Asp	Thr	Arg	Phe	Ala	Asn	His	Asn	Gln	Gly	Asn	Glu	Asp	Pro	Thr	Ala
			245						250					255	
Gly	Gly	Arg	Tyr	Ala	Val	Gln	Ser	Tyr	Leu	Glu	His	Gln	Gly	Asp	Lys
			260					265					270		
Leu	Leu	Ser	Arg	Phe	Asp	Ala	Gly	Ser	Tyr	Val	Ile	Leu	Thr	Glu	Ala
		275					280					285			
Leu	Asn	Ser	His	Asp	Val	Gly	Arg	Gly	Arg	Gly	Gly	Val	Ser	Ala	Ala
	290					295					300				
Leu	Arg	Ala	Cys	Pro	Val	Pro	Val	Val	Val	Gly	Gly	Ile	Thr	Ser	Asp
305					310					315					320
Arg	Leu	Tyr	Pro	Leu	Arg	Leu	Gln	Gln	Glu	Leu	Ala	Asp	Leu	Leu	Pro
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Gly	Cys	Ala	Gly	Leu	Arg	Val	Val	Glu	Ser	Val	Tyr	Gly	His	Asp	Gly
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Phe	Leu	Val	Glu	Thr	Glu	Ala	Val	Gly	Glu	Leu	Ile	Arg	Gln	Thr	Leu
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<210> 7

<211> 972

<212> DNA

<213> Chlorobium tepidum

<220>

<221> CDS

<222> (1)..(969)

<223> RCL01447

<400> 7

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1

5

10

15

aac gtg att ctg gtc tgc cac gcg ctg acc ggc aac gcc gac gcc gac 96

Asn	Val	Ile	Leu	Val	Cys	His	Ala	Leu	Thr	Gly	Asn	Ala	Asp	Ala	Asp	
			20					25					30			
agc	tgg	tgg	tgc	ggc	atg	ttc	ggg	gag	gga	cgg	gcg	ttc	gac	gag	act	144
Ser	Trp	Trp	Cys	Gly	Met	Phe	Gly	Glu	Gly	Arg	Ala	Phe	Asp	Glu	Thr	
		35					40					45				
cgg	gac	ttc	atc	gta	tgc	agc	aac	gtg	ctt	gga	agc	tgc	tac	gga	acg	192
Arg	Asp	Phe	Ile	Val	Cys	Ser	Asn	Val	Leu	Gly	Ser	Cys	Tyr	Gly	Thr	
	50					55					60					
acc	ggg	cgg	atg	tcg	gtg	aac	ccg	ctg	agt	ggc	agg	cac	tac	ggg	ccc	240
Thr	Gly	Pro	Met	Ser	Val	Asn	Pro	Leu	Ser	Gly	Arg	His	Tyr	Gly	Pro	
	65				70					75					80	
gat	ttt	cgg	cgc	att	acc	att	cgc	gac	atg	gtg	aac	gtt	cag	cga	tta	288
Asp	Phe	Pro	Arg	Ile	Thr	Ile	Arg	Asp	Met	Val	Asn	Val	Gln	Arg	Leu	
				85					90					95		
ttg	ctt	cgt	tcg	ctc	ggc	atc	gac	cgg	atc	cgg	ctc	atc	gtt	ggg	gca	336
Leu	Leu	Arg	Ser	Leu	Gly	Ile	Asp	Arg	Ile	Arg	Leu	Ile	Val	Gly	Ala	
			100					105					110			
tcg	ctt	ggc	ggg	atg	cag	gtg	ctc	gaa	tgg	ggc	gca	atg	tat	ccc	gaa	384
Ser	Leu	Gly	Gly	Met	Gln	Val	Leu	Glu	Trp	Gly	Ala	Met	Tyr	Pro	Glu	
		115					120				125					
atg	gcc	ggg	gcg	ctg	atg	ccg	atg	ggc	gtt	tcg	ggg	cgt	cat	tcg	gcg	432
Met	Ala	Gly	Ala	Leu	Met	Pro	Met	Gly	Val	Ser	Gly	Arg	His	Ser	Ala	
	130					135					140					
tgg	tgc	atc	gcg	cag	agc	gag	gcg	cag	cgg	cag	gct	atc	gcc	gcc	gat	480
Trp	Cys	Ile	Ala	Gln	Ser	Glu	Ala	Gln	Arg	Gln	Ala	Ile	Ala	Ala	Asp	
	145				150				155						160	
gcg	gag	tgg	caa	gat	ggc	tgg	tat	gat	ccg	gag	gtg	cag	cca	cgc	aaa	528
Ala	Glu	Trp	Gln	Asp	Gly	Trp	Tyr	Asp	Pro	Glu	Val	Gln	Pro	Arg	Lys	
			165						170				175			
gga	ctt	gcc	gcc	gcg	cgg	atg	atg	gcg	atg	tgc	acc	tac	cgc	tgc	ttc	576
Gly	Leu	Ala	Ala	Ala	Arg	Met	Met	Ala	Met	Cys	Thr	Tyr	Arg	Cys	Phe	
			180					185					190			
gag	aac	tac	cag	caa	cgc	ttt	ggc	cgc	aag	cag	cgc	gag	gac	ggc	ttg	624
Glu	Asn	Tyr	Gln	Gln	Arg	Phe	Gly	Arg	Lys	Gln	Arg	Glu	Asp	Gly	Leu	
		195					200					205				
ttc	gaa	gcc	gaa	agc	tac	gtg	cgt	cac	cag	ggc	gac	aag	ctg	gtt	ggg	672
Phe	Glu	Ala	Glu	Ser	Tyr	Val	Arg	His	Gln	Gly	Asp	Lys	Leu	Val	Gly	
	210					215					220					
cgc	ttt	gat	gca	aac	acc	tat	atc	acg	ctc	acc	aga	gcg	atg	gac	atg	720
Arg	Phe	Asp	Ala	Asn	Thr	Tyr	Ile	Thr	Leu	Thr	Arg	Ala	Met	Asp	Met	
	225				230					235					240	
cac	gac	ctc	ggg	cgc	gga	cgc	gac	tcc	tac	gaa	gcg	gcg	ctc	gga	gcg	768
His	Asp	Leu	Gly	Arg	Gly	Arg	Asp	Ser	Tyr	Glu	Ala	Ala	Leu	Gly	Ala	
			245						250					255		
ctg	aag	atg	ccg	gtc	gag	att	ctc	tcc	atc	gac	tcg	gac	gtg	ctc	tat	816
Leu	Lys	Met	Pro	Val	Glu	Ile	Leu	Ser	Ile	Asp	Ser	Asp	Val	Leu	Tyr	
			260					265					270			
ccc	agg	cag	gag	cag	gag	gaa	ctt	gcc	cgc	ctc	att	ccc	ggc	tca	cgc	864
Pro	Arg	Gln	Glu	Gln	Glu	Glu	Leu	Ala	Arg	Leu	Ile	Pro	Gly	Ser	Arg	
		275					280					285				

ctg ctt ttc ctt gac gaa ccc tat ggc cac gac gcc ttt ctt atc gac 912
 Leu Leu Phe Leu Asp Glu Pro Tyr Gly His Asp Ala Phe Leu Ile Asp
 290 295 300

acc gag acc gtc agc cgc atg gtc tgc gag ttc aag agg cag ttg ata 960
 Thr Glu Thr Val Ser Arg Met Val Cys Glu Phe Lys Arg Gln Leu Ile
 305 310 315 320

gtt gac aat tga 972
 Val Asp Asn

<210> 8
 <211> 323
 <212> PRT
 <213> Chlorobium tepidum

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Asn Val Ile Leu Val Cys His Ala Leu Thr Gly Asn Ala Asp Ala Asp
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 35 40 45

Arg Asp Phe Ile Val Cys Ser Asn Val Leu Gly Ser Cys Tyr Gly Thr
 50 55 60

Thr Gly Pro Met Ser Val Asn Pro Leu Ser Gly Arg His Tyr Gly Pro
 65 70 75 80

Asp Phe Pro Arg Ile Thr Ile Arg Asp Met Val Asn Val Gln Arg Leu
 85 90 95

Leu Leu Arg Ser Leu Gly Ile Asp Arg Ile Arg Leu Ile Val Gly Ala
 100 105 110

Ser Leu Gly Gly Met Gln Val Leu Glu Trp Gly Ala Met Tyr Pro Glu
 115 120 125

Met Ala Gly Ala Leu Met Pro Met Gly Val Ser Gly Arg His Ser Ala
 130 135 140

Trp Cys Ile Ala Gln Ser Glu Ala Gln Arg Gln Ala Ile Ala Ala Asp
 145 150 155 160

Ala Glu Trp Gln Asp Gly Trp Tyr Asp Pro Glu Val Gln Pro Arg Lys
 165 170 175

Gly Leu Ala Ala Ala Arg Met Met Ala Met Cys Thr Tyr Arg Cys Phe
 180 185 190

Glu Asn Tyr Gln Gln Arg Phe Gly Arg Lys Gln Arg Glu Asp Gly Leu
 195 200 205

Phe Glu Ala Glu Ser Tyr Val Arg His Gln Gly Asp Lys Leu Val Gly
 210 215 220

Arg Phe Asp Ala Asn Thr Tyr Ile Thr Leu Thr Arg Ala Met Asp Met
 225 230 235 240

His Asp Leu Gly Arg Gly Arg Asp Ser Tyr Glu Ala Ala Leu Gly Ala
 245 250 255

Leu Lys Met Pro Val Glu Ile Leu Ser Ile Asp Ser Asp Val Leu Tyr
 260 265 270
 Pro Arg Gln Glu Gln Glu Glu Leu Ala Arg Leu Ile Pro Gly Ser Arg
 275 280 285
 Leu Leu Phe Leu Asp Glu Pro Tyr Gly His Asp Ala Phe Leu Ile Asp
 290 295 300
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 305 310 315 320
 Val Asp Asn

<210> 9
 <211> 1149
 <212> DNA
 <213> *Caulobacter crescentus*

<220>
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 <222> (1)..(1146)
 <223> RC000727

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 ttt cct gcg aat gaa cct ctg cgg ctg gac tcc gga ggc gtc atc gaa 96
 Phe Pro Ala Asn Glu Pro Leu Arg Leu Asp Ser Gly Gly Val Ile Glu
 20 25 30

 ggt ctg gaa atc gcc tac cag acc tac ggc cag ctg aac gcg gac aag 144
 Gly Leu Glu Ile Ala Tyr Gln Thr Tyr Gly Gln Leu Asn Ala Asp Lys
 35 40 45

 tcc aac gcc gtc ctg atc tgc cac gcc ctg acg ggc gac cag cat gtg 192
 Ser Asn Ala Val Leu Ile Cys His Ala Leu Thr Gly Asp Gln His Val
 50 55 60

 gcc tcg ccc cac ccc acc acc ggc aag ccc ggc tgg tgg caa cgc ctt 240
 Ala Ser Pro His Pro Thr Thr Gly Lys Pro Gly Trp Trp Gln Arg Leu
 65 70 75 80

 gtt ggt ccc ggt aag ccg ctg gat ccc gcg cgg cac ttc atc atc tgc 288
 Val Gly Pro Gly Lys Pro Leu Asp Pro Ala Arg His Phe Ile Ile Cys
 85 90 95

 tcg aac gtg atc ggc ggc tgc atg ggc tcg acg ggc ccg gcc tcg atc 336
 Ser Asn Val Ile Gly Gly Cys Met Gly Ser Thr Gly Pro Ala Ser Ile
 100 105 110

 aat ccg gcc acg ggc aag acc tat ggc ctg tcg ttc cca gtc atc acc 384
 Asn Pro Ala Thr Gly Lys Thr Tyr Gly Leu Ser Phe Pro Val Ile Thr
 115 120 125

 atc gcc gat atg gtg cgg gcc cag gcc atg ctg gtc tct gcg ctc ggg 432
 Ile Ala Asp Met Val Arg Ala Gln Ala Met Leu Val Ser Ala Leu Gly
 130 135 140

 gtc gag acc ctg ttc gcc gtc gtc ggc ggc tcg atg ggc ggc atg cag 480
 Val Glu Thr Leu Phe Ala Val Val Gly Gly Ser Met Gly Gly Met Gln
 145 150 155 160

gtc cag caa tgg gcc gtg gac tat ccc gag cgg atg ttc agc gcc gtg 528
 Val Gln Gln Trp Ala Val Asp Tyr Pro Glu Arg Met Phe Ser Ala Val 175
 165 170

gtg ctg gcc tcg gcc tcg cgc cac tcg gcc cag aac atc gcg ttc cac 576
 Val Leu Ala Ser Ala Ser Arg His Ser Ala Gln Asn Ile Ala Phe His 190
 180 185 190

gag gtg ggc cgc cag gcg atc atg gcc gat ccc gac tgg cgc ggc ggc 624
 Glu Val Gly Arg Gln Ala Ile Met Ala Asp Pro Asp Trp Arg Gly Gly 205
 195 200

gcc tat gcc gag cac ggc gtg cgg ccc gag aag ggc ctg gcc gtg gcg 672
 Ala Tyr Ala Glu His Gly Val Arg Pro Glu Lys Gly Leu Ala Val Ala 220
 210 215

cgg atg gcc gcg cac atc acc tat ctg tcc gag ccc gcc ctg cag cgg 720
 Arg Met Ala Ala His Ile Thr Tyr Leu Ser Glu Pro Ala Leu Gln Arg 240
 225 230 235 240

aag ttc ggc cgc gag cta cag cgc gac ggc ctc tcc tgg ggc ttt gac 768
 Lys Phe Gly Arg Glu Leu Gln Arg Asp Gly Leu Ser Trp Gly Phe Asp 255
 245 250

gcc gac ttc cag gtc gag agc tat cta cgc cac cag ggg tcc agc ttc 816
 Ala Asp Phe Gln Val Glu Ser Tyr Leu Arg His Gln Gly Ser Ser Phe 270
 260 265

gtc gac cgg ttc gac gcc aac agc tat ctc tac atc acc cgg gcc atg 864
 Val Asp Arg Phe Asp Ala Asn Ser Tyr Leu Tyr Ile Thr Arg Ala Met 285
 275 280 285

gac tat ttc gac atc gcc gcc agc cat ggc ggg gtg ctg gcc aag gcg 912
 Asp Tyr Phe Asp Ile Ala Ala Ser His Gly Gly Val Leu Ala Lys Ala 300
 290 295

ttc acc cga gcg cgg aat gtg cgc ttc tgc gtg ctg agc ttc tcc agc 960
 Phe Thr Arg Ala Arg Asn Val Arg Phe Cys Val Leu Ser Phe Ser Ser 320
 305 310 315

gac tgg ctc tat ccg acc gcc gag aac cgc cac ctg gtc cgc gcc ctg 1008
 Asp Trp Leu Tyr Pro Thr Ala Glu Asn Arg His Leu Val Arg Ala Leu 335
 325 330

acc gcc gcc ggg gcc cgc gcg gcc ttc gcc gag atc gag agc gac aag 1056
 Thr Ala Ala Gly Ala Arg Ala Ala Phe Ala Glu Ile Glu Ser Asp Lys 350
 340 345

ggc cat gac gcc ttc ctg ctg gac gag ccg gtg atg gac gcc gcg ctg 1104
 Gly His Asp Ala Phe Leu Leu Asp Glu Pro Val Met Asp Ala Ala Leu 365
 355 360

gaa ggc ttc ctg gcc tcg gcc gaa cgc gat cgg ggg ctg gtt 1146
 Glu Gly Phe Leu Ala Ser Ala Glu Arg Asp Arg Gly Leu Val 380
 370 375

tga 1149

<210> 10
 <211> 382
 <212> PRT
 <213> Caulobacter crescentus

<400> 10
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Gly Leu Glu Ile Ala Tyr Gln Thr Tyr Gly Gln Leu Asn Ala Asp Lys	35	40	45
Ser Asn Ala Val Leu Ile Cys His Ala Leu Thr Gly Asp Gln His Val	50	55	60
Ala Ser Pro His Pro Thr Thr Gly Lys Pro Gly Trp Trp Gln Arg Leu	65	70	75
Val Gly Pro Gly Lys Pro Leu Asp Pro Ala Arg His Phe Ile Ile Cys	85	90	95
Ser Asn Val Ile Gly Gly Cys Met Gly Ser Thr Gly Pro Ala Ser Ile	100	105	110
Asn Pro Ala Thr Gly Lys Thr Tyr Gly Leu Ser Phe Pro Val Ile Thr	115	120	125
Ile Ala Asp Met Val Arg Ala Gln Ala Met Leu Val Ser Ala Leu Gly	130	135	140
Val Glu Thr Leu Phe Ala Val Val Gly Gly Ser Met Gly Gly Met Gln	145	150	155
Val Gln Gln Trp Ala Val Asp Tyr Pro Glu Arg Met Phe Ser Ala Val	165	170	175
Val Leu Ala Ser Ala Ser Arg His Ser Ala Gln Asn Ile Ala Phe His	180	185	190
Glu Val Gly Arg Gln Ala Ile Met Ala Asp Pro Asp Trp Arg Gly Gly	195	200	205
Ala Tyr Ala Glu His Gly Val Arg Pro Glu Lys Gly Leu Ala Val Ala	210	215	220
Arg Met Ala Ala His Ile Thr Tyr Leu Ser Glu Pro Ala Leu Gln Arg	225	230	235
Lys Phe Gly Arg Glu Leu Gln Arg Asp Gly Leu Ser Trp Gly Phe Asp	245	250	255
Ala Asp Phe Gln Val Glu Ser Tyr Leu Arg His Gln Gly Ser Ser Phe	260	265	270
Val Asp Arg Phe Asp Ala Asn Ser Tyr Leu Tyr Ile Thr Arg Ala Met	275	280	285
Asp Tyr Phe Asp Ile Ala Ala Ser His Gly Gly Val Leu Ala Lys Ala	290	295	300
Phe Thr Arg Ala Arg Asn Val Arg Phe Cys Val Leu Ser Phe Ser Ser	305	310	315
Asp Trp Leu Tyr Pro Thr Ala Glu Asn Arg His Leu Val Arg Ala Leu	325	330	335
Thr Ala Ala Gly Ala Arg Ala Ala Phe Ala Glu Ile Glu Ser Asp Lys	340	345	350
Gly His Asp Ala Phe Leu Leu Asp Glu Pro Val Met Asp Ala Ala Leu	355	360	365

Glu Gly Phe Leu Ala Ser Ala Glu Arg Asp Arg Gly Leu Val
 370 375 380

<210> 11
 <211> 1140
 <212> DNA
 <213> Neisseria gonorrhoeae

<220>
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 <222> (1)..(1137)
 <223> RNG00132

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 ttt gaa atg ccg ctg gtt ttg gaa aac ggt aaa act ttg ccg cgt ttc 96
 Phe Glu Met Pro Leu Val Leu Glu Asn Gly Lys Thr Leu Pro Arg Phe
 20 25 30
 gat ctg atg att gaa acc tac ggc gag ctg aat gct gaa aaa aac aat 144
 Asp Leu Met Ile Glu Thr Tyr Gly Glu Leu Asn Ala Glu Lys Asn Asn
 35 40 45
 gcg gtt tta atc tgc cac gcg ctg tcg ggc aac cat cac gtt gcg ggc 192
 Ala Val Leu Ile Cys His Ala Leu Ser Gly Asn His His Val Ala Gly
 50 55 60
 agg cat tcg gcg gag gat aaa tat acg ggc tgg tgg gac aat atg gtc 240
 Arg His Ser Ala Glu Asp Lys Tyr Thr Gly Trp Trp Asp Asn Met Val
 65 70 75 80
 ggt ccc gga aaa ccg att gat acg gaa cgt ttt ttc gtg gtc ggg ttg 288
 Gly Pro Gly Lys Pro Ile Asp Thr Glu Arg Phe Phe Val Val Gly Leu
 85 90 95
 aac aat ctg ggc ggc tgc gac ggc agc agc ggg cct ttg tcg atc aat 336
 Asn Asn Leu Gly Gly Cys Asp Gly Ser Ser Gly Pro Leu Ser Ile Asn
 100 105 110
 cct gaa acg ggc agg gaa tac ggc gcg gat ttt ccg atg gtt acg gtg 384
 Pro Glu Thr Gly Arg Glu Tyr Gly Ala Asp Phe Pro Met Val Thr Val
 115 120 125
 aag gac tgg gta aaa tca caa gcc gcg ctt gcc gat tat ctc ggc atc 432
 Lys Asp Trp Val Lys Ser Gln Ala Ala Leu Ala Asp Tyr Leu Gly Ile
 130 135 140
 gaa caa tgg gcg gcg gtt gtc ggc ggc agc ttg ggc ggc atg cag gct 480
 Glu Gln Trp Ala Ala Val Val Gly Gly Ser Leu Gly Gly Met Gln Ala
 145 150 155 160
 ttg cag tgg gcg att tcc tat ccc gaa cgt gtg cgc cac gcc ttg gtg 528
 Leu Gln Trp Ala Ile Ser Tyr Pro Glu Arg Val Arg His Ala Leu Val
 165 170 175
 att gcg tct gcg ccg aaa ctg tcc gcg caa aat atc gcg ttt aat gat 576
 Ile Ala Ser Ala Pro Lys Leu Ser Ala Gln Asn Ile Ala Phe Asn Asp
 180 185 190
 gta gca cgt cag gcg att ttg acc gac ccc gat ttc aat gaa gga cat 624
 Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Asp Phe Asn Glu Gly His
 195 200 205

tac cgc agc cac aac acc gtt ccc gcg cgc ggt ttg cgg att gcc cgt	672
Tyr Arg Ser His Asn Thr Val Pro Ala Arg Gly Leu Arg Ile Ala Arg	
210 215 220	
atg atg gga cac att acg tat ctt gcc gaa gac ggt ttg ggc aaa aaa	720
Met Met Gly His Ile Thr Tyr Leu Ala Glu Asp Gly Leu Gly Lys Lys	
225 230 235 240	
ttc gga cgc gat ttg cgt tcc aac ggc tat caa tac ggc tat agc gtt	768
Phe Gly Arg Asp Leu Arg Ser Asn Gly Tyr Gln Tyr Gly Tyr Ser Val	
245 250 255	
gaa ttt gaa gta gaa tcc tat ctc cgc tat caa ggc gac aaa ttc gtc	816
Glu Phe Glu Val Glu Ser Tyr Leu Arg Tyr Gln Gly Asp Lys Phe Val	
260 265 270	
ggg cgg ttt gat gct aat aca tat ttg ctg atg acc aaa gct ttg gac	864
Gly Arg Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr Lys Ala Leu Asp	
275 280 285	
tat ttc gat ccg gcg gcg gat ttc ggc aac agc ctg acc cgc gcc gtg	912
Tyr Phe Asp Pro Ala Ala Asp Phe Gly Asn Ser Leu Thr Arg Ala Val	
290 295 300	
cag gat gtg cag gca aaa ttc ttt gtc gcc agc ttc agc acc gac tgg	960
Gln Asp Val Gln Ala Lys Phe Phe Val Ala Ser Phe Ser Thr Asp Trp	
305 310 315 320	
cgt ttc gcg ccc gaa cgt tcg cac gaa ctg gtc aag gca ctg att gcc	1008
Arg Phe Ala Pro Glu Arg Ser His Glu Leu Val Lys Ala Leu Ile Ala	
325 330 335	
gcc caa aaa tcc gtg cag tat atc gaa gtc aag tcc gca cac ggc cac	1056
Ala Gln Lys Ser Val Gln Tyr Ile Glu Val Lys Ser Ala His Gly His	
340 345 350	
gat gcc ttt tta atg gaa gac gaa gcc tat atg cgc gcc gta acg gct	1104
Asp Ala Phe Leu Met Glu Asp Glu Ala Tyr Met Arg Ala Val Thr Ala	
355 360 365	
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Tyr Met Asn Asn Val Asp Lys Asp Cys Arg Leu	
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<211> 379

<212> PRT

<213> Neisseria gonorrhoeae

<400> 12

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Asp Leu Met Ile Glu Thr Tyr Gly Glu Leu Asn Ala Glu Lys Asn Asn	
35 40 45	
Ala Val Leu Ile Cys His Ala Leu Ser Gly Asn His His Val Ala Gly	
50 55 60	
Arg His Ser Ala Glu Asp Lys Tyr Thr Gly Trp Trp Asp Asn Met Val	
65 70 75 80	

Gly	Pro	Gly	Lys	Pro 85	Ile	Asp	Thr	Glu	Arg 90	Phe	Phe	Val	Val	Gly 95	Leu
Asn	Asn	Leu	Gly 100	Gly	Cys	Asp	Gly	Ser 105	Ser	Gly	Pro	Leu	Ser 110	Ile	Asn
Pro	Glu	Thr 115	Gly	Arg	Glu	Tyr	Gly 120	Ala	Asp	Phe	Pro	Met 125	Val	Thr	Val
Lys	Asp 130	Trp	Val	Lys	Ser	Gln 135	Ala	Ala	Leu	Ala	Asp 140	Tyr	Leu	Gly	Ile
Glu 145	Gln	Trp	Ala	Ala	Val 150	Val	Gly	Gly	Ser	Leu 155	Gly	Gly	Met	Gln	Ala 160
Leu	Gln	Trp	Ala	Ile 165	Ser	Tyr	Pro	Glu	Arg 170	Val	Arg	His	Ala	Leu 175	Val
Ile	Ala	Ser	Ala 180	Pro	Lys	Leu	Ser	Ala 185	Gln	Asn	Ile	Ala	Phe 190	Asn	Asp
Val	Ala	Arg 195	Gln	Ala	Ile	Leu	Thr 200	Asp	Pro	Asp	Phe	Asn 205	Glu	Gly	His
Tyr	Arg 210	Ser	His	Asn	Thr	Val 215	Pro	Ala	Arg	Gly	Leu 220	Arg	Ile	Ala	Arg
Met 225	Met	Gly	His	Ile	Thr 230	Tyr	Leu	Ala	Glu	Asp 235	Gly	Leu	Gly	Lys	Lys 240
Phe	Gly	Arg	Asp	Leu 245	Arg	Ser	Asn	Gly	Tyr 250	Gln	Tyr	Gly	Tyr	Ser 255	Val
Glu	Phe	Glu	Val 260	Glu	Ser	Tyr	Leu	Arg 265	Tyr	Gln	Gly	Asp	Lys 270	Phe	Val
Gly	Arg	Phe 275	Asp	Ala	Asn	Thr	Tyr 280	Leu	Leu	Met	Thr	Lys 285	Ala	Leu	Asp
Tyr	Phe 290	Asp	Pro	Ala	Ala	Asp 295	Phe	Gly	Asn	Ser	Leu 300	Thr	Arg	Ala	Val
Gln 305	Asp	Val	Gln	Ala	Lys 310	Phe	Phe	Val	Ala	Ser 315	Phe	Ser	Thr	Asp	Trp 320
Arg	Phe	Ala	Pro	Glu 325	Arg	Ser	His	Glu	Leu 330	Val	Lys	Ala	Leu	Ile 335	Ala
Ala	Gln	Lys	Ser 340	Val	Gln	Tyr	Ile	Glu 345	Val	Lys	Ser	Ala	His 350	Gly	His
Asp	Ala	Phe 355	Leu	Met	Glu	Asp	Glu 360	Ala	Tyr	Met	Arg	Ala 365	Val	Thr	Ala
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<210> 13
<211> 1140
<212> DNA
<213> Neisseria meningitidis ser. A
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<220>
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<222> (1)..(1137)
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<223> RNM00815

<400> 13

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ttt gaa atg ccg ctg gtt ttg gaa aac ggt aaa act ttg ccg cgt ttc	96
Phe Glu Met Pro Leu Val Leu Glu Asn Gly Lys Thr Leu Pro Arg Phe	
20 25 30	
gat ctg atg att gaa acc tac ggc gag ctg aat gcc gaa aaa aat aat	144
Asp Leu Met Ile Glu Thr Tyr Gly Glu Leu Asn Ala Glu Lys Asn Asn	
35 40 45	
gcg gtt tta atc tgt cat gcg ctg tca ggc aac cat cat gtt gcg ggc	192
Ala Val Leu Ile Cys His Ala Leu Ser Gly Asn His His Val Ala Gly	
50 55 60	
agg cat tcg gcg gag gat aaa tat acg ggc tgg tgg gac aat atg gta	240
Arg His Ser Ala Glu Asp Lys Tyr Thr Gly Trp Trp Asp Asn Met Val	
65 70 75 80	
gga ccc ggc aaa ccg att gat aca gaa cgt ttt ttc gtg gtc ggt ttg	288
Gly Pro Gly Lys Pro Ile Asp Thr Glu Arg Phe Phe Val Val Gly Leu	
85 90 95	
aac aat ctg ggc ggc tgc gac ggc agc agc gga cct ttg tcg atc aat	336
Asn Asn Leu Gly Gly Cys Asp Gly Ser Ser Gly Pro Leu Ser Ile Asn	
100 105 110	
cct gaa acg ggc agg gaa tac ggc gcg gat ttt ccg gtg gtt acg gtg	384
Pro Glu Thr Gly Arg Glu Tyr Gly Ala Asp Phe Pro Val Val Thr Val	
115 120 125	
aag gac tgg gta aaa tcc caa gcc gcg ctt acc gat tat ctc ggc atc	432
Lys Asp Trp Val Lys Ser Gln Ala Ala Leu Thr Asp Tyr Leu Gly Ile	
130 135 140	
ggg caa tgg gcg gcg gtt gtc ggc ggc agc ttg ggc ggt atg cag gct	480
Gly Gln Trp Ala Ala Val Val Gly Gly Ser Leu Gly Gly Met Gln Ala	
145 150 155 160	
ttg cag tgg acg att tcc tat ccc gag cgc gtg cgc cat gcc tta gtg	528
Leu Gln Trp Thr Ile Ser Tyr Pro Glu Arg Val Arg His Ala Leu Val	
165 170 175	
att gcg tcc gcg ccg aaa ctg tcc acg caa aat atc gcg ttt aat gat	576
Ile Ala Ser Ala Pro Lys Leu Ser Thr Gln Asn Ile Ala Phe Asn Asp	
180 185 190	
gta gca cgt cag gcg att ttg acc gat ccc gat ttc aac gaa gga cat	624
Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Asp Phe Asn Glu Gly His	
195 200 205	
tac cgc agc cgc aac acc gtt ccc gct cgg ggc ttg cgg att gcc cgc	672
Tyr Arg Ser Arg Asn Thr Val Pro Ala Arg Gly Leu Arg Ile Ala Arg	
210 215 220	
atg atg ggg cac atc acc tat ctt gcc gaa gac ggt ttg ggc aaa aaa	720
Met Met Gly His Ile Thr Tyr Leu Ala Glu Asp Gly Leu Gly Lys Lys	
225 230 235 240	
ttc gga cgc gat ttg cgt tcc aac ggc tat caa tac ggc tat ggc gtt	768
Phe Gly Arg Asp Leu Arg Ser Asn Gly Tyr Gln Tyr Gly Tyr Gly Val	
245 250 255	

gaa ttt gaa gta gaa tcc tat ctg cgc tat caa ggc gat aaa ttc gtc 816
 Glu Phe Glu Val Glu Ser Tyr Leu Arg Tyr Gln Gly Asp Lys Phe Val
 260 265 270
 ggg cgg ttt gat gcc aac acc tat ttg ctg atg acc aag gct ttg gac 864
 Gly Arg Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr Lys Ala Leu Asp
 275 280 285
 tat ttc gat ccg gcg gcg gat ttc ggc aac agc ctg acc cgc gcc gtg 912
 Tyr Phe Asp Pro Ala Ala Asp Phe Gly Asn Ser Leu Thr Arg Ala Val
 290 295 300
 cag gat gtt cag gca aaa ttc ttt gtc gcc agc ttc agc acc gat tgg 960
 Gln Asp Val Gln Ala Lys Phe Phe Val Ala Ser Phe Ser Thr Asp Trp
 305 310 315 320
 cgt ttc gcg ccc gaa cgt tcg cac gaa ctg gtc aag gcc ctg att gcc 1008
 Arg Phe Ala Pro Glu Arg Ser His Glu Leu Val Lys Ala Leu Ile Ala
 325 330 335
 gcc caa aaa tcc gtg cag tat atc gaa gtc aaa tcc gca cac ggg cac 1056
 Ala Gln Lys Ser Val Gln Tyr Ile Glu Val Lys Ser Ala His Gly His
 340 345 350
 gat gcc ttt tta atg gaa gac gaa gcc tat atg cgt gcg gtc gcc gcc 1104
 Asp Ala Phe Leu Met Glu Asp Glu Ala Tyr Met Arg Ala Val Ala Ala
 355 360 365
 tat atg aac aac gtt tat aag gaa tgt cag caa tga 1140
 Tyr Met Asn Asn Val Tyr Lys Glu Cys Gln Gln
 370 375

<210> 14

<211> 379

<212> PRT

<213> Neisseria meningitidis ser. A

<400> 14

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 Phe Glu Met Pro Leu Val Leu Glu Asn Gly Lys Thr Leu Pro Arg Phe
 20 25 30
 Asp Leu Met Ile Glu Thr Tyr Gly Glu Leu Asn Ala Glu Lys Asn Asn
 35 40 45
 Ala Val Leu Ile Cys His Ala Leu Ser Gly Asn His His Val Ala Gly
 50 55 60
 Arg His Ser Ala Glu Asp Lys Tyr Thr Gly Trp Trp Asp Asn Met Val
 65 70 75 80
 Gly Pro Gly Lys Pro Ile Asp Thr Glu Arg Phe Phe Val Val Gly Leu
 85 90 95
 Asn Asn Leu Gly Gly Cys Asp Gly Ser Ser Gly Pro Leu Ser Ile Asn
 100 105 110
 Pro Glu Thr Gly Arg Glu Tyr Gly Ala Asp Phe Pro Val Val Thr Val
 115 120 125
 Lys Asp Trp Val Lys Ser Gln Ala Ala Leu Thr Asp Tyr Leu Gly Ile
 130 135 140
 Gly Gln Trp Ala Ala Val Val Gly Gly Ser Leu Gly Gly Met Gln Ala

145	150	155	160
Leu Gln Trp Thr	Ile Ser Tyr Pro Glu Arg Val Arg His Ala Leu Val		
	165	170	175
Ile Ala Ser Ala	Pro Lys Leu Ser Thr Gln Asn Ile Ala Phe Asn Asp		
	180	185	190
Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Asp Phe Asn Glu Gly His			
	195	200	205
Tyr Arg Ser Arg Asn Thr Val Pro Ala Arg Gly Leu Arg Ile Ala Arg			
	210	215	220
Met Met Gly His Ile Thr Tyr Leu Ala Glu Asp Gly Leu Gly Lys Lys			
	225	230	235
Phe Gly Arg Asp Leu Arg Ser Asn Gly Tyr Gln Tyr Gly Tyr Gly Val			
	245	250	255
Glu Phe Glu Val Glu Ser Tyr Leu Arg Tyr Gln Gly Asp Lys Phe Val			
	260	265	270
Gly Arg Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr Lys Ala Leu Asp			
	275	280	285
Tyr Phe Asp Pro Ala Ala Asp Phe Gly Asn Ser Leu Thr Arg Ala Val			
	290	295	300
Gln Asp Val Gln Ala Lys Phe Phe Val Ala Ser Phe Ser Thr Asp Trp			
	305	310	315
Arg Phe Ala Pro Glu Arg Ser His Glu Leu Val Lys Ala Leu Ile Ala			
	325	330	335
Ala Gln Lys Ser Val Gln Tyr Ile Glu Val Lys Ser Ala His Gly His			
	340	345	350
Asp Ala Phe Leu Met Glu Asp Glu Ala Tyr Met Arg Ala Val Ala Ala			
	355	360	365
Tyr Met Asn Asn Val Tyr Lys Glu Cys Gln Gln			
	370	375	

<210> 15
 <211> 1140
 <212> DNA
 <213> Pseudomonas fluorescens

<220>
 <221> CDS
 <222> (1)..(1137)
 <223> RPU01633

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acg gcg cac ttc agc gaa ccg ctg gcc ctg gcc tgc ggc cgt tcg ctg	96
Thr Ala His Phe Ser Glu Pro Leu Ala Leu Ala Cys Gly Arg Ser Leu	
20 25 30	
gcc gat tat gac ctg atc tac gaa acc tac ggc acg ctg aac gcg caa	144
Ala Asp Tyr Asp Leu Ile Tyr Glu Thr Tyr Gly Thr Leu Asn Ala Gln	
35 40 45	

gcg	agc	aac	gcc	gtg	ctg	atc	tgc	cac	gcc	ttg	tcc	ggc	cac	cac	cat	192
Ala	Ser	Asn	Ala	Val	Leu	Ile	Cys	His	Ala	Leu	Ser	Gly	His	His	His	
	50					55					60					
gct	gcg	ggt	tat	cac	agc	gtc	gac	gac	cgc	aag	ccc	ggt	tgg	tgg	gac	240
Ala	Ala	Gly	Tyr	His	Ser	Val	Asp	Asp	Arg	Lys	Pro	Gly	Trp	Trp	Asp	
	65				70					75					80	
agc	tgc	atc	ggc	ccc	ggc	aaa	ccg	atc	gac	acc	aac	aag	ttc	ttc	gtg	288
Ser	Cys	Ile	Gly	Pro	Gly	Lys	Pro	Ile	Asp	Thr	Asn	Lys	Phe	Phe	Val	
				85					90					95		
gtc	agc	ctg	aac	ctc	ggc	ggt	tgc	aat	ggt	tct	acc	ggc	ccg	agc		336
Val	Ser	Leu	Asn	Leu	Gly	Gly	Cys	Asn	Gly	Ser	Thr	Gly	Pro	Ser		
			100				105					110				
agc	ctc	aat	ccg	gaa	acc	ggc	aag	ccg	ttc	ggc	gcc	gac	ttc	ccg	gtg	384
Ser	Leu	Asn	Pro	Glu	Thr	Gly	Lys	Pro	Phe	Gly	Ala	Asp	Phe	Pro	Val	
		115					120					125				
ctg	acc	gtg	gaa	gac	tgg	gtg	cac	agc	cag	gca	cgc	ctg	gcc	gac	ctg	432
Leu	Thr	Val	Glu	Asp	Trp	Val	His	Ser	Gln	Ala	Arg	Leu	Ala	Asp	Leu	
		130				135					140					
ctc	ggc	atc	ggc	cag	tgg	gcg	gcg	gtg	atc	ggc	ggc	agc	ctg	ggc	ggc	480
Leu	Gly	Ile	Gly	Gln	Trp	Ala	Ala	Val	Ile	Gly	Gly	Ser	Leu	Gly	Gly	
					150					155					160	
atg	cag	gcg	ctg	caa	tgg	acc	atc	acc	tat	ccg	gat	cgc	gtt	cgc	cac	528
Met	Gln	Ala	Leu	Gln	Trp	Thr	Ile	Thr	Tyr	Pro	Asp	Arg	Val	Arg	His	
				165					170					175		
tgc	ctg	gcc	atc	gcc	tcg	gcc	ccc	aag	ctg	tcg	gcg	cag	aac	atc	gcc	576
Cys	Leu	Ala	Ile	Ala	Ser	Ala	Pro	Lys	Leu	Ser	Ala	Gln	Asn	Ile	Ala	
			180					185					190			
ttc	aac	gaa	gtg	gcg	cgc	cag	gcg	atc	ctc	act	gac	ccg	gaa	ttc	cac	624
Phe	Asn	Glu	Val	Ala	Arg	Gln	Ala	Ile	Leu	Thr	Asp	Pro	Glu	Phe	His	
		195					200					205				
ggc	ggc	tcg	ttc	cag	gaa	cac	ggc	gtg	atc	ccc	aag	cgc	ggc	ctg	atg	672
Gly	Gly	Ser	Phe	Gln	Glu	His	Gly	Val	Ile	Pro	Lys	Arg	Gly	Leu	Met	
		210				215					220					
ctg	gcg	cgg	atg	gtg	ggg	cac	atc	acc	tac	ctg	tcc	gac	gac	tcc	atg	720
Leu	Ala	Arg	Met	Val	Gly	His	Ile	Thr	Tyr	Leu	Ser	Asp	Asp	Ser	Met	
					230					235					240	
ggt	gag	aaa	ttc	ggc	cgt	ggc	ctg	aag	agc	gaa	aag	ctc	aac	tac	gac	768
Gly	Glu	Lys	Phe	Gly	Arg	Gly	Leu	Lys	Ser	Glu	Lys	Leu	Asn	Tyr	Asp	
				245					250					255		
ttc	cac	agc	gtc	gag	ttc	cag	gtc	gaa	agc	tac	ctg	cgc	tat	cag	ggc	816
Phe	His	Ser	Val	Glu	Phe	Gln	Val	Glu	Ser	Tyr	Leu	Arg	Tyr	Gln	Gly	
			260					265					270			
gaa	gag	ttc	tcc	ggg	cgc	ttc	gat	gcc	aac	acc	tat	ctg	ttg	atg	acc	864
Glu	Glu	Phe	Ser	Gly	Arg	Phe	Asp	Ala	Asn	Thr	Tyr	Leu	Leu	Met	Thr	
		275					280					285				
aag	gcg	ctg	gac	tac	ttc	gat	ccg	gcg	gcg	aac	ttc	aac	gat	aac	ctg	912
Lys	Ala	Leu	Asp	Tyr	Phe	Asp	Pro	Ala	Ala	Asn	Phe	Asn	Asp	Asn	Leu	
		290				295					300					
gcg	aaa	acc	ttc	gaa	ggt	gca	aaa	gcc	aag	ttc	tgc	gtg	atg	tcg	ttc	960
Ala	Lys	Thr	Phe	Glu	Gly	Ala	Lys	Ala	Lys	Phe	Cys	Val	Met	Ser	Phe	

305	310	315	320	
acc acc gac tgg cgc ttc tcc ccg gcc cgc tcg cga gaa ctg gtg gat				1008
Thr Thr Asp Trp Arg Phe Ser Pro Ala Arg Ser Arg Glu Leu Val Asp	325	330	335	
gcg ctg atg gcg gcg cgc aaa gac gtc agc tac ctg gaa atc gac gcg				1056
Ala Leu Met Ala Ala Arg Lys Asp Val Ser Tyr Leu Glu Ile Asp Ala	340	345	350	
ccc cag ggc cac gac gcc ttc ctg att ccg atc ccg cgc tac ttg cag				1104
Pro Gln Gly His Asp Ala Phe Leu Ile Pro Ile Pro Arg Tyr Leu Gln	355	360	365	
gcg ttc ggc aat tac atg aac cgc att acg ttg tga				1140
Ala Phe Gly Asn Tyr Met Asn Arg Ile Thr Leu	370	375		

<210> 16
 <211> 379
 <212> PRT
 <213> Pseudomonas fluorescens

<400> 16
 Met Pro Ala Ala Phe Pro Pro Asp Ser Val Gly Leu Val Thr Pro Gln
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 Thr Ala His Phe Ser Glu Pro Leu Ala Leu Ala Cys Gly Arg Ser Leu
 20 25 30
 Ala Asp Tyr Asp Leu Ile Tyr Glu Thr Tyr Gly Thr Leu Asn Ala Gln
 35 40 45
 Ala Ser Asn Ala Val Leu Ile Cys His Ala Leu Ser Gly His His His
 50 55 60
 Ala Ala Gly Tyr His Ser Val Asp Asp Arg Lys Pro Gly Trp Trp Asp
 65 70 75 80
 Ser Cys Ile Gly Pro Gly Lys Pro Ile Asp Thr Asn Lys Phe Phe Val
 85 90 95
 Val Ser Leu Asn Asn Leu Gly Gly Cys Asn Gly Ser Thr Gly Pro Ser
 100 105 110
 Ser Leu Asn Pro Glu Thr Gly Lys Pro Phe Gly Ala Asp Phe Pro Val
 115 120 125
 Leu Thr Val Glu Asp Trp Val His Ser Gln Ala Arg Leu Ala Asp Leu
 130 135 140
 Leu Gly Ile Gly Gln Trp Ala Ala Val Ile Gly Gly Ser Leu Gly Gly
 145 150 155 160
 Met Gln Ala Leu Gln Trp Thr Ile Thr Tyr Pro Asp Arg Val Arg His
 165 170 175
 Cys Leu Ala Ile Ala Ser Ala Pro Lys Leu Ser Ala Gln Asn Ile Ala
 180 185 190
 Phe Asn Glu Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Glu Phe His
 195 200 205
 Gly Gly Ser Phe Gln Glu His Gly Val Ile Pro Lys Arg Gly Leu Met
 210 215 220

Leu Ala Arg Met Val Gly His Ile Thr Tyr Leu Ser Asp Asp Ser Met
 225 230 235 240
 Gly Glu Lys Phe Gly Arg Gly Leu Lys Ser Glu Lys Leu Asn Tyr Asp
 245 250 255
 Phe His Ser Val Glu Phe Gln Val Glu Ser Tyr Leu Arg Tyr Gln Gly
 260 265 270
 Glu Glu Phe Ser Gly Arg Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr
 275 280 285
 Lys Ala Leu Asp Tyr Phe Asp Pro Ala Ala Asn Phe Asn Asp Asn Leu
 290 295 300
 Ala Lys Thr Phe Glu Gly Ala Lys Ala Lys Phe Cys Val Met Ser Phe
 305 310 315 320
 Thr Thr Asp Trp Arg Phe Ser Pro Ala Arg Ser Arg Glu Leu Val Asp
 325 330 335
 Ala Leu Met Ala Ala Arg Lys Asp Val Ser Tyr Leu Glu Ile Asp Ala
 340 345 350
 Pro Gln Gly His Asp Ala Phe Leu Ile Pro Ile Pro Arg Tyr Leu Gln
 355 360 365
 Ala Phe Gly Asn Tyr Met Asn Arg Ile Thr Leu
 370 375

<210> 17

<211> 1140

<212> DNA

<213> Pseudomonas aeruginosa

<220>

<221> CDS

<222> (1)..(1137)

<223> RPA04460

<400> 17

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acg ctg cac ttc aac gaa ccg ctc gag ctg acc agc ggc aag tcc ctg	96
Thr Leu His Phe Asn Glu Pro Leu Glu Leu Thr Ser Gly Lys Ser Leu	
20 25 30	
gcc gag tac gac ctg gtg atc gaa acc tac ggc gag ctg aat gcc acg	144
Ala Glu Tyr Asp Leu Val Ile Glu Thr Tyr Gly Glu Leu Asn Ala Thr	
35 40 45	
cag agc aac gcg gtg ctg atc tgc cac gcc ctc tcc ggc cac cac cac	192
Gln Ser Asn Ala Val Leu Ile Cys His Ala Leu Ser Gly His His His	
50 55 60	
gcc gcc ggc tac cac agc gtc gac gag cgc aag ccg ggc tgg tgg gac	240
Ala Ala Gly Tyr His Ser Val Asp Glu Arg Lys Pro Gly Trp Trp Asp	
65 70 75 80	
agc tgc atc ggt ccg ggc aag ccg atc gac acc cgc aag ttc ttc gtc	288
Ser Cys Ile Gly Pro Gly Lys Pro Ile Asp Thr Arg Lys Phe Phe Val	
85 90 95	
gtc gcc ctc aac aac ctc ggc ggt tgc aac gga tcc agc ggc ccc gcc	336

Val	Ala	Leu	Asn	Asn	Leu	Gly	Gly	Cys	Asn	Gly	Ser	Ser	Gly	Pro	Ala		
			100					105					110				
agc	atc	aat	ccg	gcg	acc	ggc	aag	gtc	tac	ggc	gcg	gac	ttc	ccg	atg	384	
Ser	Ile	Asn	Pro	Ala	Thr	Gly	Lys	Val	Tyr	Gly	Ala	Asp	Phe	Pro	Met		
		115					120					125					
gtt	acg	gtg	gaa	gac	tgg	gtg	cat	agc	cag	gcg	cgc	ctg	gca	gac	cgc	432	
Val	Thr	Val	Glu	Asp	Trp	Val	His	Ser	Gln	Ala	Arg	Leu	Ala	Asp	Arg		
	130					135					140						
ctc	ggc	atc	cgc	cag	tgg	gcc	gcg	gtg	gtc	ggc	ggc	agc	ctc	ggc	ggc	480	
Leu	Gly	Ile	Arg	Gln	Trp	Ala	Ala	Val	Val	Gly	Gly	Ser	Leu	Gly	Gly		
145					150					155					160		
atg	cag	gcg	ctg	caa	tgg	acc	atc	agc	tat	ccc	gag	cgc	gtc	cgt	cac	528	
Met	Gln	Ala	Leu	Gln	Trp	Thr	Ile	Ser	Tyr	Pro	Glu	Arg	Val	Arg	His		
				165					170					175			
tgc	ctg	tgc	atc	gcc	agc	gcg	ccg	aag	ctg	tcg	gcg	cag	aac	atc	gcc	576	
Cys	Leu	Cys	Ile	Ala	Ser	Ala	Pro	Lys	Leu	Ser	Ala	Gln	Asn	Ile	Ala		
			180					185					190				
ttc	aac	gaa	gtc	gcc	cgg	cag	gcg	att	ctt	tcc	gac	cct	gag	ttc	ctc	624	
Phe	Asn	Glu	Val	Ala	Arg	Gln	Ala	Ile	Leu	Ser	Asp	Pro	Glu	Phe	Leu		
		195				200						205					
ggc	ggc	tac	ttc	cag	gag	cag	ggc	gtg	att	ccc	aag	cgc	ggc	ctc	aag	672	
Gly	Gly	Tyr	Phe	Gln	Glu	Gln	Gly	Val	Ile	Pro	Lys	Arg	Gly	Leu	Lys		
	210					215					220						
ctg	gcg	cgg	atg	gtc	ggc	cat	atc	acc	tac	ctg	tcc	gac	gac	gcc	atg	720	
Leu	Ala	Arg	Met	Val	Gly	His	Ile	Thr	Tyr	Leu	Ser	Asp	Asp	Ala	Met		
225					230					235					240		
ggc	gcc	aag	ttc	ggc	cgt	gta	ctg	aag	acc	gag	aag	ctc	aac	tac	gac	768	
Gly	Ala	Lys	Phe	Gly	Arg	Val	Leu	Lys	Thr	Glu	Lys	Leu	Asn	Tyr	Asp		
				245					250					255			
ctg	cac	agc	gtc	gag	ttc	cag	gtc	gag	agt	tac	ctg	cgc	tac	cag	ggc	816	
Leu	His	Ser	Val	Glu	Phe	Gln	Val	Glu	Ser	Tyr	Leu	Arg	Tyr	Gln	Gly		
			260					265					270				
gag	gag	ttc	tcc	acc	cgc	ttc	gac	gcc	aat	acc	tac	ctg	ctg	atg	acc	864	
Glu	Glu	Phe	Ser	Thr	Arg	Phe	Asp	Ala	Asn	Thr	Tyr	Leu	Leu	Met	Thr		
		275					280					285					
aag	gcg	ctg	gac	tac	ttc	gac	ccc	gcc	gcc	gcc	cac	ggc	gac	gac	ctg	912	
Lys	Ala	Leu	Asp	Tyr	Phe	Asp	Pro	Ala	Ala	Ala	His	Gly	Asp	Asp	Leu		
		290				295					300						
gtg	cgc	acc	ctg	gag	ggc	gtc	gag	gcg	gac	ttc	tgc	ctg	atg	tcc	ttc	960	
Val	Arg	Thr	Leu	Glu	Gly	Val	Glu	Ala	Asp	Phe	Cys	Leu	Met	Ser	Phe		
305					310					315					320		
acc	acc	gac	tgg	cgt	ttc	tcg	ccg	gcc	cgc	tcg	cgg	gaa	atc	gtc	gac	1008	
Thr	Thr	Asp	Trp	Arg	Phe	Ser	Pro	Ala	Arg	Ser	Arg	Glu	Ile	Val	Asp		
				325					330					335			
gcc	ctg	atc	gcg	gcy	aaa	aag	aac	gtc	agc	tac	ctg	gag	atc	gac	gcc	1056	
Ala	Leu	Ile	Ala	Ala	Lys	Lys	Asn	Val	Ser	Tyr	Leu	Glu	Ile	Asp	Ala		
			340					345					350				
ccg	caa	ggc	cac	gac	gcc	ttc	ctc	atg	ccg	atc	ccc	cgg	tac	ctg	caa	1104	
Pro	Gln	Gly	His	Asp	Ala	Phe	Leu	Met	Pro	Ile	Pro	Arg	Tyr	Leu	Gln		
		355					360					365					

gcc ttc agc ggt tac atg aac cgc atc agc gtg tga
 Ala Phe Ser Gly Tyr Met Asn Arg Ile Ser Val
 370 375

1140

<210> 18
 <211> 379
 <212> PRT
 <213> *Pseudomonas aeruginosa*

<400> 18
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 20 25 30
 Ala Glu Tyr Asp Leu Val Ile Glu Thr Tyr Gly Glu Leu Asn Ala Thr
 35 40 45
 Gln Ser Asn Ala Val Leu Ile Cys His Ala Leu Ser Gly His His His
 50 55 60
 Ala Ala Gly Tyr His Ser Val Asp Glu Arg Lys Pro Gly Trp Trp Asp
 65 70 75 80
 Ser Cys Ile Gly Pro Gly Lys Pro Ile Asp Thr Arg Lys Phe Phe Val
 85 90 95
 Val Ala Leu Asn Asn Leu Gly Gly Cys Asn Gly Ser Ser Gly Pro Ala
 100 105 110
 Ser Ile Asn Pro Ala Thr Gly Lys Val Tyr Gly Ala Asp Phe Pro Met
 115 120 125
 Val Thr Val Glu Asp Trp Val His Ser Gln Ala Arg Leu Ala Asp Arg
 130 135 140
 Leu Gly Ile Arg Gln Trp Ala Ala Val Val Gly Gly Ser Leu Gly Gly
 145 150 155 160
 Met Gln Ala Leu Gln Trp Thr Ile Ser Tyr Pro Glu Arg Val Arg His
 165 170 175
 Cys Leu Cys Ile Ala Ser Ala Pro Lys Leu Ser Ala Gln Asn Ile Ala
 180 185 190
 Phe Asn Glu Val Ala Arg Gln Ala Ile Leu Ser Asp Pro Glu Phe Leu
 195 200 205
 Gly Gly Tyr Phe Gln Glu Gln Gly Val Ile Pro Lys Arg Gly Leu Lys
 210 215 220
 Leu Ala Arg Met Val Gly His Ile Thr Tyr Leu Ser Asp Asp Ala Met
 225 230 235 240
 Gly Ala Lys Phe Gly Arg Val Leu Lys Thr Glu Lys Leu Asn Tyr Asp
 245 250 255
 Leu His Ser Val Glu Phe Gln Val Glu Ser Tyr Leu Arg Tyr Gln Gly
 260 265 270
 Glu Glu Phe Ser Thr Arg Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr
 275 280 285
 Lys Ala Leu Asp Tyr Phe Asp Pro Ala Ala Ala His Gly Asp Asp Leu
 290 295 300

Val Arg Thr Leu Glu Gly Val Glu Ala Asp Phe Cys Leu Met Ser Phe
 305 310 315 320

Thr Thr Asp Trp Arg Phe Ser Pro Ala Arg Ser Arg Glu Ile Val Asp
 325 330 335

Ala Leu Ile Ala Ala Lys Lys Asn Val Ser Tyr Leu Glu Ile Asp Ala
 340 345 350

Pro Gln Gly His Asp Ala Phe Leu Met Pro Ile Pro Arg Tyr Leu Gln
 355 360 365

Ala Phe Ser Gly Tyr Met Asn Arg Ile Ser Val
 370 375

<210> 19
 <211> 1146
 <212> DNA
 <213> Burkholderia cepacia

<220>
 <221> CDS
 <222> (1)..(1143)
 <223> RBU12675

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 Met Glu Ser Ile Gly Ile Val Ala Pro Gln Lys Met His Phe Thr Glu
 1 5 10 15

ccg ctg ccg ttg cag aac ggc agt tcg ctc gcc ggt tac gac ctg atg 96
 Pro Leu Pro Leu Gln Asn Gly Ser Ser Leu Ala Gly Tyr Asp Leu Met
 20 25 30

gtc gag acc tac ggc acg ctc aac gcc gcg cgt agc aac gcg gtg ctg 144
 Val Glu Thr Tyr Gly Thr Leu Asn Ala Ala Arg Ser Asn Ala Val Leu
 35 40 45

gtg tgc cac gcg ctc aac gcg tcg cac cac gtg gcg ggc gtg tat gcc 192
 Val Cys His Ala Leu Asn Ala Ser His His Val Ala Gly Val Tyr Ala
 50 55 60

gac aac ccc agg gac atc ggc tgg tgg gac aac atg gtc ggc ccg ggc 240
 Asp Asn Pro Arg Asp Ile Gly Trp Trp Asp Asn Met Val Gly Pro Gly
 65 70 75 80

aag ccg ctc gac act gac aag ttc ttc gtg atc ggc gtg aac aac ctc 288
 Lys Pro Leu Asp Thr Asp Lys Phe Phe Val Ile Gly Val Asn Asn Leu
 85 90 95

gga tcg tgc ttc ggc tcg act ggg ccg atg agc atc gat ccg tct acc 336
 Gly Ser Cys Phe Gly Ser Thr Gly Pro Met Ser Ile Asp Pro Ser Thr
 100 105 110

ggc aat ccg tac ggc gcg acg ttt ccc gtc gtg acg gtg gaa gac tgg 384
 Gly Asn Pro Tyr Gly Ala Thr Phe Pro Val Val Thr Val Glu Asp Trp
 115 120 125

gtc aac gcc cag gcg cgc gtc gcg gat caa ttc ggc atc acg cgc ttt 432
 Val Asn Ala Gln Ala Arg Val Ala Asp Gln Phe Gly Ile Thr Arg Phe
 130 135 140

gcg gcg gtg atg ggc ggc agc ctc ggc ggc atg cag gcg ctc gcg tgg 480
 Ala Ala Val Met Gly Gly Ser Leu Gly Gly Met Gln Ala Leu Ala Trp
 145 150 155 160

agc atg atg tat ccg gag cgc gtc gct cac tgc atc gtg gtc gcg tcc 528
 Ser Met Met Tyr Pro Glu Arg Val Ala His Cys Ile Val Val Ala Ser
 165 170 175

aca ccc aag ctg tcg gcg cag aac atc gcg ttc aac gag gtt gcg cgc 576
 Thr Pro Lys Leu Ser Ala Gln Asn Ile Ala Phe Asn Glu Val Ala Arg
 180 185 190

tcg gcg atc ctg tcg gac ccg gac ttc cac ggc ggc aac tac tac gcg 624
 Ser Ala Ile Leu Ser Asp Pro Asp Phe His Gly Gly Asn Tyr Tyr Ala
 195 200 205

cac aac gtt aag ccg aag cgc ggc ctg cgc gtc gcg cgc atg atc ggc 672
 His Asn Val Lys Pro Lys Arg Gly Leu Arg Val Ala Arg Met Ile Gly
 210 215 220

cac atc acg tat ctg tcg gac gac gac atg gcc gag aaa ttc ggc cgc 720
 His Ile Thr Tyr Leu Ser Asp Asp Asp Met Ala Glu Lys Phe Gly Arg
 225 230 235 240

tcg ctg cgg cgc gcg gaa ggc gcg ctg gac gcg tac aac ttc aac ttc 768
 Ser Leu Arg Arg Ala Glu Gly Ala Leu Asp Ala Tyr Asn Phe Asn Phe
 245 250 255

gac gtg gag ttc gag gtg gag tcg tac ctg cgc tac cag ggc gac aag 816
 Asp Val Glu Phe Glu Val Glu Ser Tyr Leu Arg Tyr Gln Gly Asp Lys
 260 265 270

ttc gcc gac tac ttc gac gcg aat acg tat ctg ctg atc acc cgc gcg 864
 Phe Ala Asp Tyr Phe Asp Ala Asn Thr Tyr Leu Leu Ile Thr Arg Ala
 275 280 285

ctc gac tac ttc gat ccg gcc aag gcc ttc gcc ggc gac ctg acg gcc 912
 Leu Asp Tyr Phe Asp Pro Ala Lys Ala Phe Ala Gly Asp Leu Thr Ala
 290 295 300

gcg gtc gcg cac acc acg gcg aaa tat ctg atc gcc agc ttc acg acc 960
 Ala Val Ala His Thr Ala Lys Tyr Leu Ile Ala Ser Phe Thr Thr
 305 310 315 320

gac tgg cgc ttc gcg ccg gcc cgc tcg cgt gaa ctg gtg aag gcg ctg 1008
 Asp Trp Arg Phe Ala Pro Ala Arg Ser Arg Glu Leu Val Lys Ala Leu
 325 330 335

ctc gat cac aag cgc acg gtc acc tac gcg gaa atc gac gcg ccg cac 1056
 Leu Asp His Lys Arg Thr Val Thr Tyr Ala Glu Ile Asp Ala Pro His
 340 345 350

ggc cac gac gcc ttc ctg ctc gac gac gcg cgc tat cac aac ctg atg 1104
 Gly His Asp Ala Phe Leu Leu Asp Asp Ala Arg Tyr His Asn Leu Met
 355 360 365

cgc gct tac tac gaa cgt att gcg aac gag gtg aac gca tga 1146
 Arg Ala Tyr Tyr Glu Arg Ile Ala Asn Glu Val Asn Ala
 370 375 380

<210> 20

<211> 381

<212> PRT

<213> Burkholderia cepacia

<400> 20

Met Glu Ser Ile Gly Ile Val Ala Pro Gln Lys Met His Phe Thr Glu
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Pro Leu Pro Leu Gln Asn Gly Ser Ser Leu Ala Gly Tyr Asp Leu Met
 20 25 30
 Val Glu Thr Tyr Gly Thr Leu Asn Ala Ala Arg Ser Asn Ala Val Leu
 35 40 45
 Val Cys His Ala Leu Asn Ala Ser His His Val Ala Gly Val Tyr Ala
 50 55 60
 Asp Asn Pro Arg Asp Ile Gly Trp Trp Asp Asn Met Val Gly Pro Gly
 65 70 75 80
 Lys Pro Leu Asp Thr Asp Lys Phe Phe Val Ile Gly Val Asn Asn Leu
 85 90 95
 Gly Ser Cys Phe Gly Ser Thr Gly Pro Met Ser Ile Asp Pro Ser Thr
 100 105 110
 Gly Asn Pro Tyr Gly Ala Thr Phe Pro Val Val Thr Val Glu Asp Trp
 115 120 125
 Val Asn Ala Gln Ala Arg Val Ala Asp Gln Phe Gly Ile Thr Arg Phe
 130 135 140
 Ala Ala Val Met Gly Gly Ser Leu Gly Gly Met Gln Ala Leu Ala Trp
 145 150 155 160
 Ser Met Met Tyr Pro Glu Arg Val Ala His Cys Ile Val Val Ala Ser
 165 170 175
 Thr Pro Lys Leu Ser Ala Gln Asn Ile Ala Phe Asn Glu Val Ala Arg
 180 185 190
 Ser Ala Ile Leu Ser Asp Pro Asp Phe His Gly Gly Asn Tyr Tyr Ala
 195 200 205
 His Asn Val Lys Pro Lys Arg Gly Leu Arg Val Ala Arg Met Ile Gly
 210 215 220
 His Ile Thr Tyr Leu Ser Asp Asp Asp Met Ala Glu Lys Phe Gly Arg
 225 230 235 240
 Ser Leu Arg Arg Ala Glu Gly Ala Leu Asp Ala Tyr Asn Phe Asn Phe
 245 250 255
 Asp Val Glu Phe Glu Val Glu Ser Tyr Leu Arg Tyr Gln Gly Asp Lys
 260 265 270
 Phe Ala Asp Tyr Phe Asp Ala Asn Thr Tyr Leu Leu Ile Thr Arg Ala
 275 280 285
 Leu Asp Tyr Phe Asp Pro Ala Lys Ala Phe Ala Gly Asp Leu Thr Ala
 290 295 300
 Ala Val Ala His Thr Thr Ala Lys Tyr Leu Ile Ala Ser Phe Thr Thr
 305 310 315 320
 Asp Trp Arg Phe Ala Pro Ala Arg Ser Arg Glu Leu Val Lys Ala Leu
 325 330 335
 Leu Asp His Lys Arg Thr Val Thr Tyr Ala Glu Ile Asp Ala Pro His
 340 345 350
 Gly His Asp Ala Phe Leu Leu Asp Asp Ala Arg Tyr His Asn Leu Met
 355 360 365
 Arg Ala Tyr Tyr Glu Arg Ile Ala Asn Glu Val Asn Ala

370

375

380

<210> 21
 <211> 1134
 <212> DNA
 <213> Nitrosomonas europaea

<220>
 <221> CDS
 <222> (1)..(1131)
 <223> RNE02005

<400> 21

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Met Ser Thr Gln Asp Ser Asp Ser Ile Gly Ile Val Ser Ala Arg Arg	
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gcc cat ttc gac acc ccg ctc agc ctg aaa agc gga gct gta ctg gac	96
Ala His Phe Asp Thr Pro Leu Ser Leu Lys Ser Gly Ala Val Leu Asp	
20 25 30	
agc tac gag ctc gtc tat gaa acc tat ggg gag ctg aat gca gac cga	144
Ser Tyr Glu Leu Val Tyr Glu Thr Tyr Gly Glu Leu Asn Ala Asp Arg	
35 40 45	
tcc aat gca gtg ctg atc tgc cat gct tta tcc ggc aac cac cat gtt	192
Ser Asn Ala Val Leu Ile Cys His Ala Leu Ser Gly Asn His His Val	
50 55 60	
gcc ggt gtt tat gca gat aac ccc aag aat acc gga tgg tgg aac aac	240
Ala Gly Val Tyr Ala Asp Asn Pro Lys Asn Thr Gly Trp Trp Asn Asn	
65 70 75 80	
atg atc ggt ccg ggc aaa ccg gtc gat acc cga aaa ttc ttt gtc atc	288
Met Ile Gly Pro Gly Lys Pro Val Asp Thr Arg Lys Phe Phe Val Ile	
85 90 95	
ggt atc aat aat ctc ggg ggt tgc cat ggc tcc acc ggg ccc atc agc	336
Gly Ile Asn Asn Leu Gly Gly Cys His Gly Ser Thr Gly Pro Ile Ser	
100 105 110	
atc aac gac aag acc ggt aaa cgc ttc ggc ccg gat ttt ccg ctg gta	384
Ile Asn Asp Lys Thr Gly Lys Arg Phe Gly Pro Asp Phe Pro Leu Val	
115 120 125	
acg aca gct gac tgg gca aaa acc tat gtc cgt ttc gcc gat cag ttc	432
Thr Thr Ala Asp Trp Ala Lys Thr Tyr Val Arg Phe Ala Asp Gln Phe	
130 135 140	
agc atc gac tgt ttt gcc gcc gtc atc ggt ggc agt ctg ggc ggg atg	480
Ser Ile Asp Cys Phe Ala Ala Val Ile Gly Gly Ser Leu Gly Gly Met	
145 150 155 160	
tcg gcc atg caa ctg gcg ctc gat gca ccg gaa aga gtt cgt cat gcc	528
Ser Ala Met Gln Leu Ala Leu Asp Ala Pro Glu Arg Val Arg His Ala	
165 170 175	
ata gtg gtt gca gca tcg gcc agg ctg aca gca cag aac atc gct ttc	576
Ile Val Val Ala Ala Ser Ala Arg Leu Thr Ala Gln Asn Ile Ala Phe	
180 185 190	
aat gat gtc gcg cgt cag gcg att ctg acc gac cct gat ttt cac gac	624
Asn Asp Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Asp Phe His Asp	
195 200 205	
ggc gac tat tat tcc cat ggc acc cac ccg cgc aga ggt tta cgc ctt	672

Gly	Asp	Tyr	Tyr	Ser	His	Gly	Thr	His	Pro	Arg	Arg	Gly	Leu	Arg	Leu		
210						215					220						
gcc	cgc	atg	ctt	ggc	cac	atc	acc	tac	ctg	tcg	gac	gac	tcc	atg	gcc	720	
Ala	Arg	Met	Leu	Gly	His	Ile	Thr	Tyr	Leu	Ser	Asp	Asp	Ser	Met	Ala		
225					230				235						240		
agc	aaa	ttc	ggc	cgt	gag	tta	cgt	aac	ggc	tcg	ctt	gct	ttc	aat	tat	768	
Ser	Lys	Phe	Gly	Arg	Glu	Leu	Arg	Asn	Gly	Ser	Leu	Ala	Phe	Asn	Tyr		
				245				250						255			
gat	gtg	gaa	ttc	cag	atc	gaa	tcc	tat	ctg	cac	cat	cag	ggc	gac	aaa	816	
Asp	Val	Glu	Phe	Gln	Ile	Glu	Ser	Tyr	Leu	His	His	Gln	Gly	Asp	Lys		
			260					265					270				
ttt	gcc	gac	ctg	ttc	gac	gca	aac	act	tat	ctg	ctg	atg	acg	aag	gcg	864	
Phe	Ala	Asp	Leu	Phe	Asp	Ala	Asn	Thr	Tyr	Leu	Leu	Met	Thr	Lys	Ala		
		275					280					285					
ctc	gat	tat	ttc	gat	ccg	gcc	cag	gat	tac	gat	ggc	aac	ctg	agt	gca	912	
Leu	Asp	Tyr	Phe	Asp	Pro	Ala	Gln	Asp	Tyr	Asp	Gly	Asn	Leu	Ser	Ala		
	290					295					300						
gcc	ttt	gcc	cgt	gca	caa	gcg	gat	ttt	ctg	gta	ctt	tcc	ttt	act	tcc	960	
Ala	Phe	Ala	Arg	Ala	Gln	Ala	Asp	Phe	Leu	Val	Leu	Ser	Phe	Thr	Ser		
305					310				315						320		
gac	tgg	cgt	ttt	tcc	ccg	gag	cgt	tcg	cgc	gat	atc	gtc	aag	gca	ctg	1008	
Asp	Trp	Arg	Phe	Ser	Pro	Glu	Arg	Ser	Arg	Asp	Ile	Val	Lys	Ala	Leu		
				325				330						335			
ctc	gac	aac	aaa	ctg	aat	gtc	agt	tat	gcg	gaa	att	ccc	tcc	tcg	tac	1056	
Leu	Asp	Asn	Lys	Leu	Asn	Val	Ser	Tyr	Ala	Glu	Ile	Pro	Ser	Ser	Tyr		
			340					345					350				
gga	cat	gat	tcc	ttt	ctc	atg	cag	gac	gac	tac	tat	cac	cag	ttg	ata	1104	
Gly	His	Asp	Ser	Phe	Leu	Met	Gln	Asp	Asp	Tyr	Tyr	His	Gln	Leu	Ile		
		355					360					365					
cgt	gct	tac	atg	aac	aat	atc	gct	ctc	tag							1134	
Arg	Ala	Tyr	Met	Asn	Asn	Ile	Ala	Leu									
	370					375											

<210> 22

<211> 377

<212> PRT

<213> Nitrosomonas europaea

<400> 22

Met	Ser	Thr	Gln	Asp	Ser	Asp	Ser	Ile	Gly	Ile	Val	Ser	Ala	Arg	Arg
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Ala	His	Phe	Asp	Thr	Pro	Leu	Ser	Leu	Lys	Ser	Gly	Ala	Val	Leu	Asp
			20				25					30			

Ser	Tyr	Glu	Leu	Val	Tyr	Glu	Thr	Tyr	Gly	Glu	Leu	Asn	Ala	Asp	Arg
		35				40						45			

Ser	Asn	Ala	Val	Leu	Ile	Cys	His	Ala	Leu	Ser	Gly	Asn	His	His	Val
	50					55					60				

Ala	Gly	Val	Tyr	Ala	Asp	Asn	Pro	Lys	Asn	Thr	Gly	Trp	Trp	Asn	Asn
65					70					75					80

Met	Ile	Gly	Pro	Gly	Lys	Pro	Val	Asp	Thr	Arg	Lys	Phe	Phe	Val	Ile
				85					90					95	

Gly Ile Asn Asn Leu Gly Gly Cys His Gly Ser Thr Gly Pro Ile Ser
 100 105 110
 Ile Asn Asp Lys Thr Gly Lys Arg Phe Gly Pro Asp Phe Pro Leu Val
 115 120 125
 Thr Thr Ala Asp Trp Ala Lys Thr Tyr Val Arg Phe Ala Asp Gln Phe
 130 135 140
 Ser Ile Asp Cys Phe Ala Ala Val Ile Gly Gly Ser Leu Gly Gly Met
 145 150 155 160
 Ser Ala Met Gln Leu Ala Leu Asp Ala Pro Glu Arg Val Arg His Ala
 165 170 175
 Ile Val Val Ala Ala Ser Ala Arg Leu Thr Ala Gln Asn Ile Ala Phe
 180 185 190
 Asn Asp Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Asp Phe His Asp
 195 200 205
 Gly Asp Tyr Tyr Ser His Gly Thr His Pro Arg Arg Gly Leu Arg Leu
 210 215 220
 Ala Arg Met Leu Gly His Ile Thr Tyr Leu Ser Asp Asp Ser Met Ala
 225 230 235 240
 Ser Lys Phe Gly Arg Glu Leu Arg Asn Gly Ser Leu Ala Phe Asn Tyr
 245 250 255
 Asp Val Glu Phe Gln Ile Glu Ser Tyr Leu His His Gln Gly Asp Lys
 260 265 270
 Phe Ala Asp Leu Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr Lys Ala
 275 280 285
 Leu Asp Tyr Phe Asp Pro Ala Gln Asp Tyr Asp Gly Asn Leu Ser Ala
 290 295 300
 Ala Phe Ala Arg Ala Gln Ala Asp Phe Leu Val Leu Ser Phe Thr Ser
 305 310 315 320
 Asp Trp Arg Phe Ser Pro Glu Arg Ser Arg Asp Ile Val Lys Ala Leu
 325 330 335
 Leu Asp Asn Lys Leu Asn Val Ser Tyr Ala Glu Ile Pro Ser Ser Tyr
 340 345 350
 Gly His Asp Ser Phe Leu Met Gln Asp Asp Tyr Tyr His Gln Leu Ile
 355 360 365
 Arg Ala Tyr Met Asn Asn Ile Ala Leu
 370 375

<210> 23
 <211> 1077
 <212> DNA
 <213> Haemophilus influenzae

<220>
 <221> CDS
 <222> (1)..(1074)
 <223> RHI02681

<400> 23

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1 5 10 15	
atg ctt ggc ggc aaa ctt tcc cat att aat gtc gcg tat caa act tat	96
Met Leu Gly Gly Lys Leu Ser His Ile Asn Val Ala Tyr Gln Thr Tyr	
20 25 30	
ggc acg ctc aat gcc gaa aaa aat aat gcg gta tta att tgc cac gct	144
Gly Thr Leu Asn Ala Glu Lys Asn Asn Ala Val Leu Ile Cys His Ala	
35 40 45	
ttg act ggt gat gct gag cct tat ttc gat gat ggt cga gat ggc tgg	192
Leu Thr Gly Asp Ala Glu Pro Tyr Phe Asp Asp Gly Arg Asp Gly Trp	
50 55 60	
tgg cag aat ttt atg gga gca ggt tta gca ttg gat acg gat cgt tat	240
Trp Gln Asn Phe Met Gly Ala Gly Leu Ala Leu Asp Thr Asp Arg Tyr	
65 70 75 80	
ttt ttt att agc tcg aac gta tta ggt ggt tgc aag gga aca act ggg	288
Phe Phe Ile Ser Ser Asn Val Leu Gly Gly Cys Lys Gly Thr Thr Gly	
85 90 95	
cct tca tca att aat ccg caa acg ggt aaa cct tat ggc agc caa ttt	336
Pro Ser Ser Ile Asn Pro Gln Thr Gly Lys Pro Tyr Gly Ser Gln Phe	
100 105 110	
cct aat att gtt gtg caa gat att gtt aaa gta caa aaa gcc ttg ctt	384
Pro Asn Ile Val Val Gln Asp Ile Val Lys Val Gln Lys Ala Leu Leu	
115 120 125	
gat cat ctt ggt att agc cat tta aaa gcc att att ggt gga tct ttt	432
Asp His Leu Gly Ile Ser His Leu Lys Ala Ile Ile Gly Gly Ser Phe	
130 135 140	
ggc ggc atg caa gcg aat caa tgg gcg att gat tat cct gat ttt atg	480
Gly Gly Met Gln Ala Asn Gln Trp Ala Ile Asp Tyr Pro Asp Phe Met	
145 150 155 160	
gat aat atc gtg aat ctt tgc tca tcc att tat ttt agt gct gaa gcc	528
Asp Asn Ile Val Asn Leu Cys Ser Ser Ile Tyr Phe Ser Ala Glu Ala	
165 170 175	
ata ggt ttt aat cac gta atg cgt caa gcg gtc att aat gat ccc aat	576
Ile Gly Phe Asn His Val Met Arg Gln Ala Val Ile Asn Asp Pro Asn	
180 185 190	
ttt aac ggc ggc gat tat tat gag ggt aca ccg cca gat caa ggg tta	624
Phe Asn Gly Gly Asp Tyr Tyr Glu Gly Thr Pro Pro Asp Gln Gly Leu	
195 200 205	
tct att gca cgt atg cta ggt atg ctg act tac cgc acc gat tta caa	672
Ser Ile Ala Arg Met Leu Gly Met Leu Thr Tyr Arg Thr Asp Leu Gln	
210 215 220	
ctt gcg aaa gcc ttt ggg cgt gcc aca aaa tca gat ggc agc ttt tgg	720
Leu Ala Lys Ala Phe Gly Arg Ala Thr Lys Ser Asp Gly Ser Phe Trp	
225 230 235 240	
ggc gat tac ttt caa gtg gaa tcc tat ctt tct tac caa ggc aaa aaa	768
Gly Asp Tyr Phe Gln Val Glu Ser Tyr Leu Ser Tyr Gln Gly Lys Lys	
245 250 255	
ttc tta gaa cgt ttt gat gcc aat agt tat ttg cat ttg tta cgt gcg	816
Phe Leu Glu Arg Phe Asp Ala Asn Ser Tyr Leu His Leu Arg Ala	
260 265 270	

ttg gat atg tat gat cca agt ttg ggg tat gac aat gtt aaa gag gca 864
 Leu Asp Met Tyr Asp Pro Ser Leu Gly Tyr Asp Asn Val Lys Glu Ala
 275 280 285
 tta tca cgt att aaa gca cgc tat acg ttg gtt tct gtg aca acg gat 912
 Leu Ser Arg Ile Lys Ala Arg Tyr Thr Leu Val Ser Val Thr Thr Asp
 290 295 300
 caa ctt ttt aaa ccc att gat ctt tat aaa agt aaa cag ctt tta gag 960
 Gln Leu Phe Lys Pro Ile Asp Leu Tyr Lys Ser Lys Gln Leu Leu Glu
 305 310 315 320
 caa agt gga gtc gat cta cat ttt tat gaa ttc cca tca gat tac gga 1008
 Gln Ser Gly Val Asp Leu His Phe Tyr Glu Phe Pro Ser Asp Tyr Gly
 325 330 335
 cac gat gcg ttt tta gtg gat tat gat cag ttt gaa aaa cga att cga 1056
 His Asp Ala Phe Leu Val Asp Tyr Asp Gln Phe Glu Lys Arg Ile Arg
 340 345 350
 gat ggt ttg gca ggt aat taa 1077
 Asp Gly Leu Ala Gly Asn
 355

<210> 24
 <211> 358
 <212> PRT
 <213> Haemophilus influenzae

<400> 24
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 20 25 30
 Gly Thr Leu Asn Ala Glu Lys Asn Asn Ala Val Leu Ile Cys His Ala
 35 40 45
 Leu Thr Gly Asp Ala Glu Pro Tyr Phe Asp Asp Gly Arg Asp Gly Trp
 50 55 60
 Trp Gln Asn Phe Met Gly Ala Gly Leu Ala Leu Asp Thr Asp Arg Tyr
 65 70 75 80
 Phe Phe Ile Ser Ser Asn Val Leu Gly Gly Cys Lys Gly Thr Thr Gly
 85 90 95
 Pro Ser Ser Ile Asn Pro Gln Thr Gly Lys Pro Tyr Gly Ser Gln Phe
 100 105 110
 Pro Asn Ile Val Val Gln Asp Ile Val Lys Val Gln Lys Ala Leu Leu
 115 120 125
 Asp His Leu Gly Ile Ser His Leu Lys Ala Ile Ile Gly Gly Ser Phe
 130 135 140
 Gly Gly Met Gln Ala Asn Gln Trp Ala Ile Asp Tyr Pro Asp Phe Met
 145 150 155 160
 Asp Asn Ile Val Asn Leu Cys Ser Ser Ile Tyr Phe Ser Ala Glu Ala
 165 170 175
 Ile Gly Phe Asn His Val Met Arg Gln Ala Val Ile Asn Asp Pro Asn
 180 185 190

Phe Asn Gly Gly Asp Tyr Tyr Glu Gly Thr Pro Pro Asp Gln Gly Leu
 195 200 205
 Ser Ile Ala Arg Met Leu Gly Met Leu Thr Tyr Arg Thr Asp Leu Gln
 210 215 220
 Leu Ala Lys Ala Phe Gly Arg Ala Thr Lys Ser Asp Gly Ser Phe Trp
 225 230 235 240
 Gly Asp Tyr Phe Gln Val Glu Ser Tyr Leu Ser Tyr Gln Gly Lys Lys
 245 250 255
 Phe Leu Glu Arg Phe Asp Ala Asn Ser Tyr Leu His Leu Leu Arg Ala
 260 265 270
 Leu Asp Met Tyr Asp Pro Ser Leu Gly Tyr Asp Asn Val Lys Glu Ala
 275 280 285
 Leu Ser Arg Ile Lys Ala Arg Tyr Thr Leu Val Ser Val Thr Thr Asp
 290 295 300
 Gln Leu Phe Lys Pro Ile Asp Leu Tyr Lys Ser Lys Gln Leu Leu Glu
 305 310 315 320
 Gln Ser Gly Val Asp Leu His Phe Tyr Glu Phe Pro Ser Asp Tyr Gly
 325 330 335
 His Asp Ala Phe Leu Val Asp Tyr Asp Gln Phe Glu Lys Arg Ile Arg
 340 345 350
 Asp Gly Leu Ala Gly Asn
 355

<210> 25
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 <212> DNA
 <213> Halobacterium sp

<220>
 <221> CDS
 <222> (1)..(1293)
 <223> ETX_HALN1

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 Met Gly His Asp His Gly Leu His Thr Asn Ser Val His Ala Gly Gln
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 cgc gtc gac ccg gcc acg ggc gct cgc gcg ccg cca ctc tac cag acc 96
 Arg Val Asp Pro Ala Thr Gly Ala Arg Ala Pro Pro Leu Tyr Gln Thr
 20 25 30
 acg tcg tac gcc ttc gag gac agc gcc gat gcc gcc ggc cag ttc gcc 144
 Thr Ser Tyr Ala Phe Glu Asp Ser Ala Asp Ala Ala Gly Gln Phe Ala
 35 40 45
 ctt gag cgg gac ggc tac atc tac tcg cgg ctg atg aac ccc acc gtg 192
 Leu Glu Arg Asp Gly Tyr Ile Tyr Ser Arg Leu Met Asn Pro Thr Val
 50 55 60
 gag acc ctc cag gac cgc ctc gcc gcc ctc gaa ggc ggc gtc ggc gcg 240
 Glu Thr Leu Gln Asp Arg Leu Ala Ala Leu Glu Gly Gly Val Gly Ala
 65 70 75 80
 gtc gcc acc gcg tcc gga atg gcc gcc ctg gac ctc gcg acg ttc ctg 288

Val	Ala	Thr	Ala	Ser	Gly	Met	Ala	Ala	Leu	Asp	Leu	Ala	Thr	Phe	Leu	
				85					90					95		
ctg	gca	cgc	gcc	ggc	gac	tcc	gtc	gtc	gcc	gcc	agc	gac	ctc	tac	ggc	336
Leu	Ala	Arg	Ala	Gly	Asp	Ser	Val	Val	Ala	Ala	Ser	Asp	Leu	Tyr	Gly	
			100					105					110			
ggc	acc	gtg	acg	tac	ctc	acg	cac	agc	gcc	cag	cgc	cgc	ggc	gtc	gac	384
Gly	Thr	Val	Thr	Tyr	Leu	Thr	His	Ser	Ala	Gln	Arg	Arg	Gly	Val	Asp	
		115					120					125				
acg	acg	ttc	gtg	gac	gtc	ctc	gac	tac	gac	gcc	tac	gcc	gac	gcc	atc	432
Thr	Thr	Phe	Val	Asp	Val	Leu	Asp	Tyr	Asp	Ala	Tyr	Ala	Asp	Ala	Ile	
	130					135					140					
gac	gcc	gac	acc	gcc	tac	gtg	ctc	gtc	gaa	acc	gtc	ggc	aac	ccc	agc	480
Asp	Ala	Asp	Thr	Ala	Tyr	Val	Leu	Val	Glu	Thr	Val	Gly	Asn	Pro	Ser	
145					150					155					160	
ctg	atc	acg	ccc	gac	ctc	gaa	cgc	atc	gcc	gac	atc	gcc	cac	gac	aac	528
Leu	Ile	Thr	Pro	Asp	Leu	Glu	Arg	Ile	Ala	Asp	Ile	Ala	His	Asp	Asn	
				165					170					175		
ggc	gtt	ccc	ctg	ctg	gtg	gac	aac	acg	ttc	gcg	acc	ccc	gcg	ctg	gca	576
Gly	Val	Pro	Leu	Leu	Val	Asp	Asn	Thr	Phe	Ala	Thr	Pro	Ala	Leu	Ala	
			180					185					190			
acc	ccg	atc	gac	cac	ggt	gcc	gac	atc	gtc	tgg	cac	tcc	acc	acc	aaa	624
Thr	Pro	Ile	Asp	His	Gly	Ala	Asp	Ile	Val	Trp	His	Ser	Thr	Thr	Lys	
		195					200					205				
tgg	atc	cac	ggt	gcc	ggc	acc	acc	gtc	ggc	ggc	gcg	ctc	gtc	gac	gcc	672
Trp	Ile	His	Gly	Ala	Gly	Thr	Thr	Val	Gly	Gly	Ala	Leu	Val	Asp	Ala	
	210					215					220					
ggc	agc	ttc	gac	tgg	gac	gcc	cac	gcc	gcc	gac	tac	ccc	gag	atc	gcc	720
Gly	Ser	Phe	Asp	Trp	Asp	Ala	His	Ala	Ala	Asp	Tyr	Pro	Glu	Ile	Ala	
225					230					235					240	
cag	gaa	aac	ccc	gcc	tac	cac	ggc	gtg	acc	ttc	acc	gat	cgc	ttc	ggg	768
Gln	Glu	Asn	Pro	Ala	Tyr	His	Gly	Val	Thr	Phe	Thr	Asp	Arg	Phe	Gly	
				245					250					255		
gac	gcc	gcg	ttc	acg	tac	gcc	gca	atc	gcc	cgc	ggg	ctg	cgc	gat	ctg	816
Asp	Ala	Ala	Phe	Thr	Tyr	Ala	Ala	Ile	Ala	Arg	Gly	Leu	Arg	Asp	Leu	
			260					265					270			
ggc	aac	cag	cag	tcg	ccg	ttc	gac	gcc	tgg	cag	acc	ctc	cag	aag	ctc	864
Gly	Asn	Gln	Gln	Ser	Pro	Phe	Asp	Ala	Trp	Gln	Thr	Leu	Gln	Lys	Leu	
		275					280					285				
gaa	acg	ctc	ccg	ctg	cgc	atg	caa	caa	cac	tgc	cgg	aac	gcc	cag	ctc	912
Glu	Thr	Leu	Pro	Leu	Arg	Met	Gln	Gln	His	Cys	Arg	Asn	Ala	Gln	Leu	
	290					295					300					
gtc	gcc	gaa	cac	ctc	cgg	gac	cac	ccc	aac	gtg	tcg	tgg	gtc	aac	tac	960
Val	Ala	Glu	His	Leu	Arg	Asp	His	Pro	Asn	Val	Ser	Trp	Val	Asn	Tyr	
305					310					315					320	
ccc	ggg	ctg	gcc	gac	cac	gac	acc	cac	gac	aac	gca	acc	acc	tac	ctc	1008
Pro	Gly	Leu	Ala	Asp	His	Asp	Thr	His	Asp	Asn	Ala	Thr	Thr	Tyr	Leu	
				325					330					335		
gat	tcg	ggc	tac	gga	ggc	atg	ctc	acg	ttc	ggc	gtc	gag	gac	ggc	tac	1056
Asp	Ser	Gly	Tyr	Gly	Gly	Met	Leu	Thr	Phe	Gly	Val	Glu	Asp	Gly	Tyr	
			340					345					350			

gag gcc gcc caa tcg gtc acc gag gag acc acg ctt gcc agc ctg ctg 1104
 Glu Ala Ala Gln Ser Val Thr Glu Glu Thr Thr Leu Ala Ser Leu Leu
 355 360 365

gcg aac gtc ggc gac gcc aaa acg ctc gtg atc cac ccc gcc tcc acc 1152
 Ala Asn Val Gly Asp Ala Lys Thr Leu Val Ile His Pro Ala Ser Thr
 370 375 380

acc cac cag cag ctc acc ccc gaa gcc cag cgc gcc ggc ggt gtg cgc 1200
 Thr His Gln Gln Leu Thr Pro Glu Ala Gln Arg Ala Gly Gly Val Arg
 385 390 395 400

ccc gag atg gtg cgg gtg tcg gtc ggc atc gag gac ccc gcc gac atc 1248
 Pro Glu Met Val Arg Val Ser Val Gly Ile Glu Asp Pro Ala Asp Ile
 405 410 415

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tag 1296

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 <213> Halobacterium sp

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Thr Ser Tyr Ala Phe Glu Asp Ser Ala Asp Ala Ala Gly Gln Phe Ala
 35 40 45

Leu Glu Arg Asp Gly Tyr Ile Tyr Ser Arg Leu Met Asn Pro Thr Val
 50 55 60

Glu Thr Leu Gln Asp Arg Leu Ala Ala Leu Glu Gly Gly Val Gly Ala
 65 70 75 80

Val Ala Thr Ala Ser Gly Met Ala Ala Leu Asp Leu Ala Thr Phe Leu
 85 90 95

Leu Ala Arg Ala Gly Asp Ser Val Val Ala Ala Ser Asp Leu Tyr Gly
 100 105 110

Gly Thr Val Thr Tyr Leu Thr His Ser Ala Gln Arg Arg Gly Val Asp
 115 120 125

Thr Thr Phe Val Asp Val Leu Asp Tyr Asp Ala Tyr Ala Asp Ala Ile
 130 135 140

Asp Ala Asp Thr Ala Tyr Val Leu Val Glu Thr Val Gly Asn Pro Ser
 145 150 155 160

Leu Ile Thr Pro Asp Leu Glu Arg Ile Ala Asp Ile Ala His Asp Asn
 165 170 175

Gly Val Pro Leu Leu Val Asp Asn Thr Phe Ala Thr Pro Ala Leu Ala
 180 185 190

Thr Pro Ile Asp His Gly Ala Asp Ile Val Trp His Ser Thr Thr Lys
 195 200 205

Trp Ile His Gly Ala Gly Thr Thr Val Gly Gly Ala Leu Val Asp Ala
 210 215 220
 Gly Ser Phe Asp Trp Asp Ala His Ala Ala Asp Tyr Pro Glu Ile Ala
 225 230 235 240
 Gln Glu Asn Pro Ala Tyr His Gly Val Thr Phe Thr Asp Arg Phe Gly
 245 250 255
 Asp Ala Ala Phe Thr Tyr Ala Ala Ile Ala Arg Gly Leu Arg Asp Leu
 260 265 270
 Gly Asn Gln Gln Ser Pro Phe Asp Ala Trp Gln Thr Leu Gln Lys Leu
 275 280 285
 Glu Thr Leu Pro Leu Arg Met Gln Gln His Cys Arg Asn Ala Gln Leu
 290 295 300
 Val Ala Glu His Leu Arg Asp His Pro Asn Val Ser Trp Val Asn Tyr
 305 310 315 320
 Pro Gly Leu Ala Asp His Asp Thr His Asp Asn Ala Thr Thr Tyr Leu
 325 330 335
 Asp Ser Gly Tyr Gly Gly Met Leu Thr Phe Gly Val Glu Asp Gly Tyr
 340 345 350
 Glu Ala Ala Gln Ser Val Thr Glu Glu Thr Thr Leu Ala Ser Leu Leu
 355 360 365
 Ala Asn Val Gly Asp Ala Lys Thr Leu Val Ile His Pro Ala Ser Thr
 370 375 380
 Thr His Gln Gln Leu Thr Pro Glu Ala Gln Arg Ala Gly Gly Val Arg
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 <222> (1)..(1140)
 <223> RTT00268

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 Leu Lys Pro Pro Arg Ser Pro Leu Ser Ile Pro Pro Pro Lys Pro Arg
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 acc gcc gtc ctc ttc ccc agg cgg gag ggg ttc tac acg gag ctc ggg 144
 Thr Ala Val Leu Phe Pro Arg Arg Glu Gly Phe Tyr Thr Glu Leu Gly
 35 40 45

ggg tac ctc ccc gag gtg cgc ctc cgc ttt gag acc tac ggg acc ctc	192
Gly Tyr Leu Pro Glu Val Arg Leu Arg Phe Glu Thr Tyr Gly Thr Leu	
50 55 60	
tcc cgc agg cgg gat aac gcc gtc ctc gtc ttc cac gcc ctc acg ggg	240
Ser Arg Arg Arg Asp Asn Ala Val Leu Val Phe His Ala Leu Thr Gly	
65 70 75 80	
agc gcc cac ctg gcg ggg acc tac gac gag gaa acc ttt aga agc ctc	288
Ser Ala His Leu Ala Gly Thr Tyr Asp Glu Thr Phe Arg Ser Leu	
85 90 95	
tcc ccc ctg gag cag gcc ttc ggc cgg gaa ggg tgg tgg gac agc ctg	336
Ser Pro Leu Glu Gln Ala Phe Gly Arg Glu Gly Trp Trp Asp Ser Leu	
100 105 110	
gtg ggg ccc ggg cgg atc ctg gac ccc gcc ctc tac tac gtg gtc tcc	384
Val Gly Pro Gly Arg Ile Leu Asp Pro Ala Leu Tyr Tyr Val Val Ser	
115 120 125	
gcc aac cac ctg gga agc tgc tac ggc tcc acc ggc ccc ctc tcc cta	432
Ala Asn His Leu Gly Ser Cys Tyr Gly Ser Thr Gly Pro Leu Ser Leu	
130 135 140	
gac ccc cac acg ggc cgc ccc tac ggg agg gac ttc cct ccc ctt acc	480
Asp Pro His Thr Gly Arg Pro Tyr Gly Arg Asp Phe Pro Pro Leu Thr	
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atc cgc gac ctg gcc cgg gcc cag gcg agg ctt ctg gac cat ctg ggg	528
Ile Arg Asp Leu Ala Arg Ala Gln Ala Arg Leu Leu Asp His Leu Gly	
165 170 175	
gtg gag aag gcc atc gtc atc ggg ggg agc ctc ggg ggg atg gtg gcc	576
Val Glu Lys Ala Ile Val Ile Gly Gly Ser Leu Gly Gly Met Val Ala	
180 185 190	
ctg gag ttc gcc ctc atg tac ccg gag agg gtg aag aag ctc gtg gtc	624
Leu Glu Phe Ala Leu Met Tyr Pro Glu Arg Val Lys Lys Leu Val Val	
195 200 205	
ctg gcg gcc ccc gca cgg cac ggc ccc tgg gcc cgg gcc ttc aac cac	672
Leu Ala Ala Pro Ala Arg His Gly Pro Trp Ala Arg Ala Phe Asn His	
210 215 220	
ctc tcc cgc cag gcc atc ctc caa gac ccc gag tac cag aag ggc aac	720
Leu Ser Arg Gln Ala Ile Leu Gln Asp Pro Glu Tyr Gln Lys Gly Asn	
225 230 235 240	
cct gcc ccc aag ggc atg gcc ctc gcc cgg gga atc gcc atg atg agc	768
Pro Ala Pro Lys Gly Met Ala Leu Ala Arg Gly Ile Ala Met Met Ser	
245 250 255	
tac cgg gcc ccc gag ggg ttt gag gcc cgc tgg ggc gcg gag ccc gag	816
Tyr Arg Ala Pro Glu Gly Phe Glu Ala Arg Trp Gly Ala Glu Pro Glu	
260 265 270	
ctc ggg gaa atc cac ctg gac tac cag ggg gag aag ttc ctc cgg cgc	864
Leu Gly Glu Ile His Leu Asp Tyr Gln Gly Glu Lys Phe Leu Arg Arg	
275 280 285	
ttc cac gcc gag agc tac ctc gtc ctc tcc cgg gcc atg gac aac cac	912
Phe His Ala Glu Ser Tyr Leu Val Leu Ser Arg Ala Met Asp Asn His	
290 295 300	
gac gtg ggc cgg ggc cgg ggc ggg gtg gag gag gcc ctg aag cgc ctc	960
Asp Val Gly Arg Gly Arg Gly Gly Val Glu Glu Ala Leu Lys Arg Leu	
305 310 315 320	

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agg gcc atc ccc tcc ctc ttc gtg ggc att gac acc gac ctc ctc tac 1008
Arg Ala Ile Pro Ser Leu Phe Val Gly Ile Asp Thr Asp Leu Leu Tyr
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ccc gcc tgg gag gtg agg cag gcg gcc aag gcg gcg ggg gcc cgc tac 1056
Pro Ala Trp Glu Val Arg Gln Ala Ala Lys Ala Ala Gly Ala Arg Tyr
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cgg gag atc aaa agc ccc cac ggg cac gac gcc ttc ctc ata gag acc 1104
Arg Glu Ile Lys Ser Pro His Gly His Asp Ala Phe Leu Ile Glu Thr
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gac cag gtg gag gag atc ctg gac gcc ttc ctc ccg tag 1143
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<210> 28

<211> 380

<212> PRT

<213> Thermus thermophilus

<400> 28

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Thr Ala Val Leu Phe Pro Arg Arg Glu Gly Phe Tyr Thr Glu Leu Gly
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Gly Tyr Leu Pro Glu Val Arg Leu Arg Phe Glu Thr Tyr Gly Thr Leu
               50               55               60

Ser Arg Arg Arg Asp Asn Ala Val Leu Val Phe His Ala Leu Thr Gly
  65               70               75               80

Ser Ala His Leu Ala Gly Thr Tyr Asp Glu Glu Thr Phe Arg Ser Leu
               85               90               95

Ser Pro Leu Glu Gln Ala Phe Gly Arg Glu Gly Trp Trp Asp Ser Leu
               100              105              110

Val Gly Pro Gly Arg Ile Leu Asp Pro Ala Leu Tyr Tyr Val Val Ser
               115              120              125

Ala Asn His Leu Gly Ser Cys Tyr Gly Ser Thr Gly Pro Leu Ser Leu
               130              135              140

Asp Pro His Thr Gly Arg Pro Tyr Gly Arg Asp Phe Pro Pro Leu Thr
  145              150              155              160

Ile Arg Asp Leu Ala Arg Ala Gln Ala Arg Leu Leu Asp His Leu Gly
               165              170              175

Val Glu Lys Ala Ile Val Ile Gly Gly Ser Leu Gly Gly Met Val Ala
               180              185              190

Leu Glu Phe Ala Leu Met Tyr Pro Glu Arg Val Lys Lys Leu Val Val
               195              200              205

Leu Ala Ala Pro Ala Arg His Gly Pro Trp Ala Arg Ala Phe Asn His
               210              215              220

Leu Ser Arg Gln Ala Ile Leu Gln Asp Pro Glu Tyr Gln Lys Gly Asn

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225	230					235					240				
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Tyr	Arg	Ala	Pro	Glu	Gly	Phe	Glu	Ala	Arg	Trp	Gly	Ala	Glu	Pro	Glu
			260					265					270		
Leu	Gly	Glu	Ile	His	Leu	Asp	Tyr	Gln	Gly	Glu	Lys	Phe	Leu	Arg	Arg
		275					280					285			
Phe	His	Ala	Glu	Ser	Tyr	Leu	Val	Leu	Ser	Arg	Ala	Met	Asp	Asn	His
	290					295					300				
Asp	Val	Gly	Arg	Gly	Arg	Gly	Gly	Val	Glu	Glu	Ala	Leu	Lys	Arg	Leu
305					310					315					320
Arg	Ala	Ile	Pro	Ser	Leu	Phe	Val	Gly	Ile	Asp	Thr	Asp	Leu	Leu	Tyr
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Pro	Ala	Trp	Glu	Val	Arg	Gln	Ala	Ala	Lys	Ala	Ala	Gly	Ala	Arg	Tyr
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Arg	Glu	Ile	Lys	Ser	Pro	His	Gly	His	Asp	Ala	Phe	Leu	Ile	Glu	Thr
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 <213> *Deinococcus radiodurans*

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 <222> (1)..(1002)
 <223> RDR01287

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1				5				10						15					
gaa	ccc	gac	tgt	tcg	ggg	ccg	cag	acg	gtc	gtt	ctc	ttc	cgg	cgt	gag				96
Glu	Pro	Asp	Cys	Ser	Gly	Pro	Gln	Thr	Val	Val	Leu	Phe	Arg	Arg	Glu				
			20					25					30						
ccg	ctg	ctg	ctc	gac	tgc	gga	cgg	gcg	ctg	agc	gac	gtg	cgg	gtg	gcc				144
Pro	Leu	Leu	Leu	Asp	Cys	Gly	Arg	Ala	Leu	Ser	Asp	Val	Arg	Val	Ala				
			35				40					45							
ttt	cac	acc	tac	ggc	acg	ccg	cgc	gcc	gac	gcc	acg	ctg	gtg	ctg	cac				192
Phe	His	Thr	Tyr	Gly	Thr	Pro	Arg	Ala	Asp	Ala	Thr	Leu	Val	Leu	His				
			50			55					60								
gcc	ctg	acc	ggc	gac	agc	gcg	gtg	cac	gag	tgg	tgg	ccc	gac	ttt	ctg				240
Ala	Leu	Thr	Gly	Asp	Ser	Ala	Val	His	Glu	Trp	Trp	Pro	Asp	Phe	Leu				
	65				70					75					80				
ggc	gcg	ggc	cgg	cca	ctg	gac	ccg	gca	gac	gac	tac	gtg	gtg	tgc	gcc				288
Gly	Ala	Gly	Arg	Pro	Leu	Asp	Pro	Ala	Asp	Asp	Tyr	Val	Val	Cys	Ala				
				85					90					95					
aac	gtc	ctc	ggc	ggg	tgc	gcc	ggc	acg	acg	agc	gcc	gct	gaa	ctc	gcc				336
Asn	Val	Leu	Gly	Gly	Cys	Ala	Gly	Thr	Thr	Ser	Ala	Ala	Glu	Leu	Ala				

100										105										110										
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Ala	Thr	Cys	Ser	Gly	Pro	Val	Pro	Leu	Ser	Leu	Arg	Asp	Met	Ala	Arg															
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Val	Gly	Arg	Ala	Leu	Leu	Asp	Ser	Leu	Gly	Val	Arg	Arg	Val	Arg	Val															
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Ile	Gly	Ala	Ser	Met	Gly	Gly	Met	Leu	Ala	Tyr	Ala	Trp	Leu	Leu	Glu															
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tgc	ccc	gac	ctg	gtg	gaa	aag	gcc	gtg	att	ata	gga	gcc	ccg	gcg	cgg	528														
Cys	Pro	Asp	Leu	Val	Glu	Lys	Ala	Val	Ile	Ile	Gly	Ala	Pro	Ala	Arg															
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cac	tcg	ccc	tgg	gct	att	gga	ctg	aac	acg	gcg	gcc	cgc	agc	gcc	att	576														
His	Ser	Pro	Trp	Ala	Ile	Gly	Leu	Asn	Thr	Ala	Ala	Arg	Ser	Ala	Ile															
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gcc	ctc	gct	ccc	ggc	ggc	gag	ggg	ctg	aag	gtg	gcg	cgc	cag	att	gcc	624														
Ala	Leu	Ala	Pro	Gly	Gly	Glu	Gly	Leu	Lys	Val	Ala	Arg	Gln	Ile	Ala															
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Met	Leu	Ser	Tyr	Arg	Ser	Pro	Glu	Ser	Leu	Ser	Arg	Thr	Gln	Ala	Gly															
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Gln	Arg	Val	Pro	Gly	Val	Pro	Ala	Val	Thr	Ser	Tyr	Leu	His	Tyr	Gln															
225										235																				
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245										255																				
acc	tgg	gcg	atg	gac	gcc	ttt	cag	ccg	agc	agc	gcc	gac	ctc	aaa	gcg	816														
Thr	Trp	Ala	Met	Asp	Ala	Phe	Gln	Pro	Ser	Ser	Ala	Asp	Leu	Lys	Ala															
260										270																				
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Val	Arg	Ala	Pro	Val	Leu	Val	Val	Gly	Ile	Ser	Ser	Asp	Leu	Leu	Tyr															
275										285																				
ccc	gcc	gcc	gag	gtc	cgc	gcc	tgc	gcc	gcc	gag	ctt	ccc	cac	gcc	gac	912														
Pro	Ala	Ala	Glu	Val	Arg	Ala	Cys	Ala	Ala	Glu	Leu	Pro	His	Ala	Asp															
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<211> 334

<212> PRT

<213> Deinococcus radiodurans

<400> 30

M/43127

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 Phe His Thr Tyr Gly Thr Pro Arg Ala Asp Ala Thr Leu Val Leu His
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 65 70 75 80
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 85 90 95
 Asn Val Leu Gly Gly Cys Ala Gly Thr Thr Ser Ala Ala Glu Leu Ala
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 Ala Thr Cys Ser Gly Pro Val Pro Leu Ser Leu Arg Asp Met Ala Arg
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 Val Gly Arg Ala Leu Leu Asp Ser Leu Gly Val Arg Arg Val Arg Val
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 Ile Gly Ala Ser Met Gly Gly Met Leu Ala Tyr Ala Trp Leu Leu Glu
 145 150 155 160
 Cys Pro Asp Leu Val Glu Lys Ala Val Ile Ile Gly Ala Pro Ala Arg
 165 170 175
 His Ser Pro Trp Ala Ile Gly Leu Asn Thr Ala Ala Arg Ser Ala Ile
 180 185 190
 Ala Leu Ala Pro Gly Gly Glu Gly Leu Lys Val Ala Arg Gln Ile Ala
 195 200 205
 Met Leu Ser Tyr Arg Ser Pro Glu Ser Leu Ser Arg Thr Gln Ala Gly
 210 215 220
 Gln Arg Val Pro Gly Val Pro Ala Val Thr Ser Tyr Leu His Tyr Gln
 225 230 235 240
 Gly Glu Lys Leu Ala Ala Arg Phe Asp Glu Gln Thr Tyr Cys Ala Leu
 245 250 255
 Thr Trp Ala Met Asp Ala Phe Gln Pro Ser Ser Ala Asp Leu Lys Ala
 260 265 270
 Val Arg Ala Pro Val Leu Val Val Gly Ile Ser Ser Asp Leu Leu Tyr
 275 280 285
 Pro Ala Ala Glu Val Arg Ala Cys Ala Ala Glu Leu Pro His Ala Asp
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<223> RSC08123

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Ile Val Gln Val Pro Glu Leu Val Leu Glu Ser Gly Val Val Ile Asn	
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aat ttc cct att gct tat aag acg tgg ggt aca ctg aat gaa gct ggt	192
Asn Phe Pro Ile Ala Tyr Lys Thr Trp Gly Thr Leu Asn Glu Ala Gly	
50 55 60	
gat aat gtt ctg gta att tgt cat gcc ttg act ggg tcc gca gat gtt	240
Asp Asn Val Leu Val Ile Cys His Ala Leu Thr Gly Ser Ala Asp Val	
65 70 75 80	
gct gac tgg tgg ggc cct ctt ctg ggt aac gac tta gca ttc gac cca	288
Ala Asp Trp Trp Gly Pro Leu Leu Gly Asn Asp Leu Ala Phe Asp Pro	
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tca agg ttt ttt atc ata tgt tta aac tct atg ggc tct cca tat ggg	336
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Pro Glu Phe Pro Leu Cys Thr Val Arg Asp Asp Val Arg Ala His Arg	
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Ile Val Leu Asp Ser Leu Gly Val Lys Ser Ile Ala Cys Val Ile Gly	
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Gly Ser Met Gly Gly Met Leu Ser Leu Glu Trp Ala Ala Met Tyr Gly	
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Lys Glu Tyr Val Lys Asn Met Val Ala Leu Ala Thr Ser Ala Arg His	
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Ser Asp Pro Asn Tyr Leu Asp Gly Tyr Tyr Pro Val Glu Glu Gln Pro	
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Thr Arg Asn Ser Phe Glu Asn Lys Phe Ser Arg Arg Ser Pro Ser Ile	
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Ala Gln Gln Gln Lys Ala Gln Arg Glu Glu Thr Arg Lys Pro Ser Thr	
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Val Ser Glu His Ser Leu Gln Ile His Asn Asp Gly Tyr Lys Thr Lys	
275 280 285	
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Val Ser Thr Ala Ser Ser Ser Asp Ser Leu Asn Ser Ser Thr Ser Met	
305 310 315 320	
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Thr Ser Val Ser Ser Val Thr Gly Glu Val Lys Asp Ile Lys Pro Ala	
325 330 335	
cag acg tat ttt tct gca caa agt tac ttg agg tac cag ggc aca aag	1056
Gln Thr Tyr Phe Ser Ala Gln Ser Tyr Leu Arg Tyr Gln Gly Thr Lys	
340 345 350	
ttc atc aat agg ttc gac gcc aat tgt tac att gcc atc aca cgt aaa	1104
Phe Ile Asn Arg Phe Asp Ala Asn Cys Tyr Ile Ala Ile Thr Arg Lys	
355 360 365	
ctg gat acg cac gat ttg gca aga gac aga gta gat gac atc act gag	1152
Leu Asp Thr His Asp Leu Ala Arg Asp Arg Val Asp Asp Ile Thr Glu	
370 375 380	
gtc ctt tct acc atc caa caa cca tcc ctg atc atc ggt atc caa tct	1200
Val Leu Ser Thr Ile Gln Gln Pro Ser Leu Ile Ile Gly Ile Gln Ser	
385 390 395 400	
gat gga ctg ttc aca tat tca gaa caa gaa ttt ttg gct gag cac ata	1248
Asp Gly Leu Phe Thr Tyr Ser Glu Gln Glu Phe Leu Ala Glu His Ile	
405 410 415	
ccg aag tcg caa tta gaa aaa att gaa tct ccc gaa ggc cac gat gcc	1296
Pro Lys Ser Gln Leu Glu Lys Ile Glu Ser Pro Glu Gly His Asp Ala	
420 425 430	
ttc cta ttg gag ttt aag ctg ata aac aaa ctg ata gta caa ttt tta	1344
Phe Leu Leu Glu Phe Lys Leu Ile Asn Lys Leu Ile Val Gln Phe Leu	
435 440 445	
aaa acc aac tgc aag gcc att acc gat gcc gct cca aga gct tgg gga	1392
Lys Thr Asn Cys Lys Ala Ile Thr Asp Ala Ala Pro Arg Ala Trp Gly	
450 455 460	
ggc gac gtt ggt aac gat gaa acg aag acg tct gtc ttt ggt gag gcc	1440
Gly Asp Val Gly Asn Asp Glu Thr Lys Thr Ser Val Phe Gly Glu Ala	
465 470 475 480	
gaa gaa gtt acc aac tgg tag	1461
Glu Glu Val Thr Asn Trp	
485	

<210> 32

<211> 486

<212> PRT

<213> Saccharomyces cerevisiae

<400> 32

Met Ser His Thr Leu Lys Ser Lys Thr Leu Gln Glu Leu Asp Ile Glu
1 5 10 15

Glu Ile Lys Glu Thr Asn Pro Leu Leu Lys Leu Val Gln Gly Gln Arg
20 25 30

Ile Val Gln Val Pro Glu Leu Val Leu Glu Ser Gly Val Val Ile Asn
35 40 45

Asn Phe Pro Ile Ala Tyr Lys Thr Trp Gly Thr Leu Asn Glu Ala Gly
50 55 60

Asp Asn Val Leu Val Ile Cys His Ala Leu Thr Gly Ser Ala Asp Val
65 70 75 80

Ala Asp Trp Trp Gly Pro Leu Leu Gly Asn Asp Leu Ala Phe Asp Pro
85 90 95

Ser Arg Phe Phe Ile Ile Cys Leu Asn Ser Met Gly Ser Pro Tyr Gly
100 105 110

Ser Phe Ser Pro Leu Thr Ile Asn Glu Glu Thr Gly Val Arg Tyr Gly
115 120 125

Pro Glu Phe Pro Leu Cys Thr Val Arg Asp Asp Val Arg Ala His Arg
130 135 140

Ile Val Leu Asp Ser Leu Gly Val Lys Ser Ile Ala Cys Val Ile Gly
145 150 155 160

Gly Ser Met Gly Gly Met Leu Ser Leu Glu Trp Ala Ala Met Tyr Gly
165 170 175

Lys Glu Tyr Val Lys Asn Met Val Ala Leu Ala Thr Ser Ala Arg His
180 185 190

Ser Ala Trp Cys Ile Ser Trp Ser Glu Ala Gln Arg Gln Ser Ile Tyr
195 200 205

Ser Asp Pro Asn Tyr Leu Asp Gly Tyr Tyr Pro Val Glu Glu Gln Pro
210 215 220

Val Ala Gly Leu Ser Ala Ala Arg Met Ser Ala Leu Leu Thr Tyr Arg
225 230 235 240

Thr Arg Asn Ser Phe Glu Asn Lys Phe Ser Arg Arg Ser Pro Ser Ile
245 250 255

Ala Gln Gln Gln Lys Ala Gln Arg Glu Glu Thr Arg Lys Pro Ser Thr
260 265 270

Val Ser Glu His Ser Leu Gln Ile His Asn Asp Gly Tyr Lys Thr Lys
275 280 285

Ala Ser Thr Ala Ile Ala Gly Ile Ser Gly Gln Lys Gly Gln Ser Val
290 295 300

Val Ser Thr Ala Ser Ser Ser Asp Ser Leu Asn Ser Ser Thr Ser Met
305 310 315 320

Thr Ser Val Ser Ser Val Thr Gly Glu Val Lys Asp Ile Lys Pro Ala
325 330 335

Gln Thr Tyr Phe Ser Ala Gln Ser Tyr Leu Arg Tyr Gln Gly Thr Lys
 340 345 350

Phe Ile Asn Arg Phe Asp Ala Asn Cys Tyr Ile Ala Ile Thr Arg Lys
 355 360 365

Leu Asp Thr His Asp Leu Ala Arg Asp Arg Val Asp Asp Ile Thr Glu
 370 375 380

Val Leu Ser Thr Ile Gln Gln Pro Ser Leu Ile Ile Gly Ile Gln Ser
 385 390 395 400

Asp Gly Leu Phe Thr Tyr Ser Glu Gln Glu Phe Leu Ala Glu His Ile
 405 410 415

Pro Lys Ser Gln Leu Glu Lys Ile Glu Ser Pro Glu Gly His Asp Ala
 420 425 430

Phe Leu Leu Glu Phe Lys Leu Ile Asn Lys Leu Ile Val Gln Phe Leu
 435 440 445

Lys Thr Asn Cys Lys Ala Ile Thr Asp Ala Ala Pro Arg Ala Trp Gly
 450 455 460

Gly Asp Val Gly Asn Asp Glu Thr Lys Thr Ser Val Phe Gly Glu Ala
 465 470 475 480

Glu Glu Val Thr Asn Trp
 485

<210> 33
 <211> 1470
 <212> DNA
 <213> Schizosaccharomyces pombe

<220>
 <221> CDS
 <222> (1)..(1467)
 <223> RS001936

<400> 33
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 Met Glu Ser Gln Ser Pro Ile Glu Ser Ile Val Phe Thr Asp Ser Cys
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cat ccg tct cag caa gaa aat aaa ttt gtt cag ctt att tca gat caa 96
 His Pro Ser Gln Gln Glu Asn Lys Phe Val Gln Leu Ile Ser Asp Gln
 20 25 30

aaa att gca att gtt ccc aaa ttt acg ttg gag tgt ggc gac atc ctt 144
 Lys Ile Ala Ile Val Pro Lys Phe Thr Leu Glu Cys Gly Asp Ile Leu
 35 40 45

tac gat gtt ccc gtt gcc ttc aag act tgg ggt act ttg aat aaa gaa 192
 Tyr Asp Val Pro Val Ala Phe Lys Thr Trp Gly Thr Leu Asn Lys Glu
 50 55 60

gga aac aat tgt ctt ctt ctt tgt cat gct tta agt ggt tct gct gat 240
 Gly Asn Asn Cys Leu Leu Leu Cys His Ala Leu Ser Gly Ser Ala Asp
 65 70 75 80

gct gga gat tgg tgg ggt cct tta ctc ggt cct ggt cgt gcg ttt gat 288
 Ala Gly Asp Trp Trp Gly Pro Leu Leu Gly Pro Gly Arg Ala Phe Asp
 85 90 95

cca tca cat ttc ttt atc gta tgc ctt aat tct ctt ggt agc cca tac	336
Pro Ser His Phe Phe Ile Val Cys Leu Asn Ser Leu Gly Ser Pro Tyr	
100 105 110	
gga agc gcc tct cct gtt aca tgg aac gct gag act cat agt gtt tat	384
Gly Ser Ala Ser Pro Val Thr Trp Asn Ala Glu Thr His Ser Val Tyr	
115 120 125	
ggg cca gaa ttt cct tta gca acc ata cgt gat gat gta aac atc cat	432
Gly Pro Glu Phe Pro Leu Ala Thr Ile Arg Asp Asp Val Asn Ile His	
130 135 140	
aaa ctt att tta caa aga ttg ggt gta aag caa att gct atg gca gta	480
Lys Leu Ile Leu Gln Arg Leu Gly Val Lys Gln Ile Ala Met Ala Val	
145 150 155 160	
ggg ggc tcc atg ggt ggt atg ctg gtt ttg gag tgg gca ttt gat aag	528
Gly Gly Ser Met Gly Gly Met Leu Val Leu Glu Trp Ala Phe Asp Lys	
165 170 175	
gaa ttt gtg cga tca att gtt ccc att tct acc tct ctt cgt cat tcc	576
Glu Phe Val Arg Ser Ile Val Pro Ile Ser Thr Ser Leu Arg His Ser	
180 185 190	
gcg tgg tgc att agc tgg tct gaa gcg caa cgc cag agt ata tat tct	624
Ala Trp Cys Ile Ser Trp Ser Glu Ala Gln Arg Gln Ser Ile Tyr Ser	
195 200 205	
gac cct aag ttt aat gat gga tac tac ggc ata gac gat cag cct gta	672
Asp Pro Lys Phe Asn Asp Gly Tyr Tyr Gly Ile Asp Asp Gln Pro Val	
210 215 220	
agt ggc ctt gga gct gct cgt atg tct gcc ttg ttg aca tat cgc tcc	720
Ser Gly Leu Gly Ala Ala Arg Met Ser Ala Leu Leu Thr Tyr Arg Ser	
225 230 235 240	
aaa tgt tct ttc gaa cgt cgc ttt gcc cgt act gtt cct gat gcg tct	768
Lys Cys Ser Phe Glu Arg Arg Phe Ala Arg Thr Val Pro Asp Ala Ser	
245 250 255	
cgt cac ccc tat cca gat cgt tta ccc act cct ctc acg ccc agt aat	816
Arg His Pro Tyr Pro Asp Arg Leu Pro Thr Pro Leu Thr Pro Ser Asn	
260 265 270	
gca cat tgg gtc gtt cac aac gaa gga aac cgt aat cgc cgt gaa cga	864
Ala His Trp Val Val His Asn Glu Gly Asn Arg Asn Arg Arg Glu Arg	
275 280 285	
cct tgt cga tcc aat gga tca tca cct act tct gaa agt gct tta aat	912
Pro Cys Arg Ser Asn Gly Ser Ser Pro Thr Ser Glu Ser Ala Leu Asn	
290 295 300	
tcc ccc gcc tct tct gtc tgc tct tta cct tct tta ggt gcc tct cag	960
Ser Pro Ala Ser Ser Val Ser Ser Leu Pro Ser Leu Gly Ala Ser Gln	
305 310 315 320	
act aca gac agt tct tcc ctt aac cag agt tgc tta tta aga cgt cct	1008
Thr Thr Asp Ser Ser Ser Leu Asn Gln Ser Ser Leu Leu Arg Arg Pro	
325 330 335	
gct aat act tac ttc tct gcg caa tgc tat tta cgt tac caa gcg aag	1056
Ala Asn Thr Tyr Phe Ser Ala Gln Ser Tyr Leu Arg Tyr Gln Ala Lys	
340 345 350	
aag ttt gta agt cgc ttt gat gct aat tgt tac att tgc att act aaa	1104
Lys Phe Val Ser Arg Phe Asp Ala Asn Cys Tyr Ile Ser Ile Thr Lys	
355 360 365	

aag ttg gac acc cat gat att act cgt gga cgc ggt tca gac tct cct 1152
Lys Leu Asp Thr His Asp Ile Thr Arg Gly Arg Gly Ser Asp Ser Pro
370 375 380

aag gaa gtc atg aag gat ttg tct tta ccc gta ctc gta ctc ggt att 1200
Lys Glu Val Met Lys Asp Leu Ser Leu Pro Val Leu Val Leu Gly Ile
385 390 395 400

gaa agc gat ggt ctt ttc aca ttt gac gaa caa gtt gaa att gcc aaa 1248
Glu Ser Asp Gly Leu Phe Thr Phe Asp Glu Gln Val Glu Ile Ala Lys
405 410 415

tct ttt ccc aat gct acc ttg gaa aaa att att tcg gcc gaa ggc cac 1296
Ser Phe Pro Asn Ala Thr Leu Glu Lys Ile Ile Ser Ala Glu Gly His
420 425 430

gac ggt ttt ttg ctt gag ttt act caa gta aac tca cat att caa aaa 1344
Asp Gly Phe Leu Leu Glu Phe Thr Gln Val Asn Ser His Ile Gln Lys
435 440 445

ttc caa aag gaa cat tta att gat atc atg tct caa act aat tcc ttt 1392
Phe Gln Lys Glu His Leu Ile Asp Ile Met Ser Gln Thr Asn Ser Phe
450 455 460

gag cga ctt gat tcc caa gtt aat gat acc aac cgc gaa agc gtt ttt 1440
Glu Arg Leu Asp Ser Gln Val Asn Asp Thr Asn Arg Glu Ser Val Phe
465 470 475 480

gga gaa atg gaa gac ata acc tcc tgg taa 1470
Gly Glu Met Glu Asp Ile Thr Ser Trp
485

<210> 34
<211> 489
<212> PRT
<213> Schizosaccharomyces pombe

<400> 34
Met Glu Ser Gln Ser Pro Ile Glu Ser Ile Val Phe Thr Asp Ser Cys
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His Pro Ser Gln Gln Glu Asn Lys Phe Val Gln Leu Ile Ser Asp Gln
20 25 30

Lys Ile Ala Ile Val Pro Lys Phe Thr Leu Glu Cys Gly Asp Ile Leu
35 40 45

Tyr Asp Val Pro Val Ala Phe Lys Thr Trp Gly Thr Leu Asn Lys Glu
50 55 60

Gly Asn Asn Cys Leu Leu Leu Cys His Ala Leu Ser Gly Ser Ala Asp
65 70 75 80

Ala Gly Asp Trp Trp Gly Pro Leu Leu Gly Pro Gly Arg Ala Phe Asp
85 90 95

Pro Ser His Phe Phe Ile Val Cys Leu Asn Ser Leu Gly Ser Pro Tyr
100 105 110

Gly Ser Ala Ser Pro Val Thr Trp Asn Ala Glu Thr His Ser Val Tyr
115 120 125

Gly Pro Glu Phe Pro Leu Ala Thr Ile Arg Asp Asp Val Asn Ile His
130 135 140

Lys Leu Ile Leu Gln Arg Leu Gly Val Lys Gln Ile Ala Met Ala Val
 145 150 155 160
 Gly Gly Ser Met Gly Gly Met Leu Val Leu Glu Trp Ala Phe Asp Lys
 165 170 175
 Glu Phe Val Arg Ser Ile Val Pro Ile Ser Thr Ser Leu Arg His Ser
 180 185 190
 Ala Trp Cys Ile Ser Trp Ser Glu Ala Gln Arg Gln Ser Ile Tyr Ser
 195 200 205
 Asp Pro Lys Phe Asn Asp Gly Tyr Tyr Gly Ile Asp Asp Gln Pro Val
 210 215 220
 Ser Gly Leu Gly Ala Ala Arg Met Ser Ala Leu Leu Thr Tyr Arg Ser
 225 230 235 240
 Lys Cys Ser Phe Glu Arg Arg Phe Ala Arg Thr Val Pro Asp Ala Ser
 245 250 255
 Arg His Pro Tyr Pro Asp Arg Leu Pro Thr Pro Leu Thr Pro Ser Asn
 260 265 270
 Ala His Trp Val Val His Asn Glu Gly Asn Arg Asn Arg Arg Glu Arg
 275 280 285
 Pro Cys Arg Ser Asn Gly Ser Ser Pro Thr Ser Glu Ser Ala Leu Asn
 290 295 300
 Ser Pro Ala Ser Ser Val Ser Ser Leu Pro Ser Leu Gly Ala Ser Gln
 305 310 315 320
 Thr Thr Asp Ser Ser Ser Leu Asn Gln Ser Ser Leu Leu Arg Arg Pro
 325 330 335
 Ala Asn Thr Tyr Phe Ser Ala Gln Ser Tyr Leu Arg Tyr Gln Ala Lys
 340 345 350
 Lys Phe Val Ser Arg Phe Asp Ala Asn Cys Tyr Ile Ser Ile Thr Lys
 355 360 365
 Lys Leu Asp Thr His Asp Ile Thr Arg Gly Arg Gly Ser Asp Ser Pro
 370 375 380
 Lys Glu Val Met Lys Asp Leu Ser Leu Pro Val Leu Val Leu Gly Ile
 385 390 395 400
 Glu Ser Asp Gly Leu Phe Thr Phe Asp Glu Gln Val Glu Ile Ala Lys
 405 410 415
 Ser Phe Pro Asn Ala Thr Leu Glu Lys Ile Ile Ser Ala Glu Gly His
 420 425 430
 Asp Gly Phe Leu Leu Glu Phe Thr Gln Val Asn Ser His Ile Gln Lys
 435 440 445
 Phe Gln Lys Glu His Leu Ile Asp Ile Met Ser Gln Thr Asn Ser Phe
 450 455 460
 Glu Arg Leu Asp Ser Gln Val Asn Asp Thr Asn Arg Glu Ser Val Phe
 465 470 475 480
 Gly Glu Met Glu Asp Ile Thr Ser Trp
 485

<210> 35
 <211> 1113
 <212> DNA
 <213> Xylella almond

<220>
 <221> CDS
 <222> (1)..(1110)
 <223> RXFX01562

<400> 35
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 Met Thr Glu Phe Ile Pro Pro Gly Ser Leu Phe His Ala Leu Ser Ser
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cca ttt gcg atg aag cgt ggc gga caa ctc cac cac gcc cgc atc gct 96
 Pro Phe Ala Met Lys Arg Gly Gly Gln Leu His His Ala Arg Ile Ala
 20 25 30

tac gaa aca tgg ggc cgc ctc aat gcc agc gcc acc aat gcc att ctg 144
 Tyr Glu Thr Trp Gly Arg Leu Asn Ala Ser Ala Thr Asn Ala Ile Leu
 35 40 45

atc atg cct ggc tta tca ccc aat gca cat gcc gca cac cat gac agc 192
 Ile Met Pro Gly Leu Ser Pro Asn Ala His Ala Ala His His Asp Ser
 50 55 60

aat gct gag cca ggc tgg tgg gag tca atg cta ggt cca ggc aaa ccc 240
 Asn Ala Glu Pro Gly Trp Trp Glu Ser Met Leu Gly Pro Gly Lys Pro
 65 70 75 80

atc gac aca gac cgt tgg ttc gtg atc tgt gtc aac tca ctt ggt agc 288
 Ile Asp Thr Asp Arg Trp Phe Val Ile Cys Val Asn Ser Leu Gly Ser
 85 90 95

tgc aaa gga tcg act ggc cct gca tcg tac aac ccc atc acg cag gcc 336
 Cys Lys Gly Ser Thr Gly Pro Ala Ser Tyr Asn Pro Ile Thr Gln Ala
 100 105 110

atg tat cgt ttg gac ttt cca gca ctg tca atc gaa gac ggg gcc aac 384
 Met Tyr Arg Leu Asp Phe Pro Ala Leu Ser Ile Glu Asp Gly Ala Asn
 115 120 125

tcc gca att gaa gtg gta cat gca ctg ggc atc aag caa ctt gcc agc 432
 Ser Ala Ile Glu Val Val His Ala Leu Gly Ile Lys Gln Leu Ala Ser
 130 135 140

ctg atc ggc aat tca atg ggc ggc atg acg gca ctg gcc atc ctg ctg 480
 Leu Ile Gly Asn Ser Met Gly Gly Met Thr Ala Leu Ala Ile Leu Leu
 145 150 155 160

tta cat cca gat ata gcc cgc agc cac atc aac atc tca ggc agc gcg 528
 Leu His Pro Asp Ile Ala Arg Ser His Ile Asn Ile Ser Gly Ser Ala
 165 170 175

cag gca tta ccg ttt tcc atc gcc att cgc tcg cta caa cgc gag gcg 576
 Gln Ala Leu Pro Phe Ser Ile Ala Ile Arg Ser Leu Gln Arg Glu Ala
 180 185 190

atc cgc ctg gac ccc cat tgg agg cag gga gac tac gac gac acc cac 624
 Ile Arg Leu Asp Pro His Trp Arg Gln Gly Asp Tyr Asp Asp Thr His
 195 200 205

tac ccg gaa tcg ggg cta cgc atc gca cgc aaa ctt ggg gtg atc acc 672
 Tyr Pro Glu Ser Gly Leu Arg Ile Ala Arg Lys Leu Gly Val Ile Thr
 210 215 220

tac cgc tcc gcg ctg gaa tgg gac ggg cgt ttt ggc cgg gta cgc ttg 720
 Tyr Arg Ser Ala Leu Glu Trp Asp Gly Arg Phe Gly Arg Val Arg Leu
 225 230 235 240
 gat tgc gac caa acc aac gac aca cca ttc gga ctg gaa ttc caa att 768
 Asp Ser Asp Gln Thr Asn Asp Thr Pro Phe Gly Leu Glu Phe Gln Ile
 245 250 255
 gaa aac tac ttg gaa agc cat gca cac cgc ttc gtg cac acc ttc gac 816
 Glu Asn Tyr Leu Glu Ser His Ala His Arg Phe Val His Thr Phe Asp
 260 265 270
 cca aac tgc tac ctg tac ctg agc cgc tcc atg gac tgg ttc gac gtg 864
 Pro Asn Cys Tyr Leu Tyr Leu Ser Arg Ser Met Asp Trp Phe Asp Val
 275 280 285
 gcc gag tac gcc aat gga gac att ctt gcc ggg ctg gcc agg atc cga 912
 Ala Glu Tyr Ala Asn Gly Asp Ile Leu Ala Gly Leu Ala Arg Ile Arg
 290 295 300
 atc caa cgc gca ctc gcc atc ggt agc cat acc gac atc ctc ttt cca 960
 Ile Gln Arg Ala Leu Ala Ile Gly Ser His Thr Asp Ile Leu Phe Pro
 305 310 315 320
 ata caa cag caa caa caa att gcc gaa ggg cta cgc cgt ggc ggt aca 1008
 Ile Gln Gln Gln Gln Gln Ile Ala Glu Gly Leu Arg Arg Gly Gly Thr
 325 330 335
 cac gcc acc ttc ctg ggc ctt gac tca ccg cag ggg cat gat gcg ttc 1056
 His Ala Thr Phe Leu Gly Leu Asp Ser Pro Gln Gly His Asp Ala Phe
 340 345 350
 ctt gtg gat atc gca aga ttt ggc cct cca gtg aag gaa ttt ctg gac 1104
 Leu Val Asp Ile Ala Arg Phe Gly Pro Pro Val Lys Glu Phe Leu Asp
 355 360 365
 gaa ctg tga 1113
 Glu Leu
 370

<210> 36
 <211> 370
 <212> PRT
 <213> Xylella almond

<400> 36
 Met Thr Glu Phe Ile Pro Pro Gly Ser Leu Phe His Ala Leu Ser Ser
 1 5 10 15
 Pro Phe Ala Met Lys Arg Gly Gly Gln Leu His His Ala Arg Ile Ala
 20 25 30
 Tyr Glu Thr Trp Gly Arg Leu Asn Ala Ser Ala Thr Asn Ala Ile Leu
 35 40 45
 Ile Met Pro Gly Leu Ser Pro Asn Ala His Ala Ala His His Asp Ser
 50 55 60
 Asn Ala Glu Pro Gly Trp Trp Glu Ser Met Leu Gly Pro Gly Lys Pro
 65 70 75 80
 Ile Asp Thr Asp Arg Trp Phe Val Ile Cys Val Asn Ser Leu Gly Ser
 85 90 95
 Cys Lys Gly Ser Thr Gly Pro Ala Ser Tyr Asn Pro Ile Thr Gln Ala
 100 105 110

Met Tyr Arg Leu Asp Phe Pro Ala Leu Ser Ile Glu Asp Gly Ala Asn
115 120 125

Ser Ala Ile Glu Val Val His Ala Leu Gly Ile Lys Gln Leu Ala Ser
130 135 140

Leu Ile Gly Asn Ser Met Gly Gly Met Thr Ala Leu Ala Ile Leu Leu
145 150 155 160

Leu His Pro Asp Ile Ala Arg Ser His Ile Asn Ile Ser Gly Ser Ala
165 170 175

Gln Ala Leu Pro Phe Ser Ile Ala Ile Arg Ser Leu Gln Arg Glu Ala
180 185 190

Ile Arg Leu Asp Pro His Trp Arg Gln Gly Asp Tyr Asp Asp Thr His
195 200 205

Tyr Pro Glu Ser Gly Leu Arg Ile Ala Arg Lys Leu Gly Val Ile Thr
210 215 220

Tyr Arg Ser Ala Leu Glu Trp Asp Gly Arg Phe Gly Arg Val Arg Leu
225 230 235 240

Asp Ser Asp Gln Thr Asn Asp Thr Pro Phe Gly Leu Glu Phe Gln Ile
245 250 255

Glu Asn Tyr Leu Glu Ser His Ala His Arg Phe Val His Thr Phe Asp
260 265 270

Pro Asn Cys Tyr Leu Tyr Leu Ser Arg Ser Met Asp Trp Phe Asp Val
275 280 285

Ala Glu Tyr Ala Asn Gly Asp Ile Leu Ala Gly Leu Ala Arg Ile Arg
290 295 300

Ile Gln Arg Ala Leu Ala Ile Gly Ser His Thr Asp Ile Leu Phe Pro
305 310 315 320

Ile Gln Gln Gln Gln Gln Ile Ala Glu Gly Leu Arg Arg Gly Gly Thr
325 330 335

His Ala Thr Phe Leu Gly Leu Asp Ser Pro Gln Gly His Asp Ala Phe
340 345 350

Leu Val Asp Ile Ala Arg Phe Gly Pro Pro Val Lys Glu Phe Leu Asp
355 360 365

Glu Leu
370

<210> 37
<211> 1113
<212> DNA
<213> Xylella oleander

<220>
<221> CDS
<222> (1)..(1110)
<223> RXYF01729

<400> 37
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Met Thr Glu Phe Ile Pro Pro Gly Ser Leu Phe His Ala Leu Ser Ser
1 5 10 15

cca	ttt	gcg	atg	aag	cgt	ggc	gga	caa	ctc	cac	cac	gcc	cgc	atc	gct	96
Pro	Phe	Ala	Met	Lys	Arg	Gly	Gly	Gln	Leu	His	His	Ala	Arg	Ile	Ala	
			20					25					30			
tac	gaa	aca	tgg	ggc	cgc	ctc	aat	gcc	agc	gcc	acc	aat	gcc	att	ctg	144
Tyr	Glu	Thr	Trp	Gly	Arg	Leu	Asn	Ala	Ser	Ala	Thr	Asn	Ala	Ile	Leu	
		35					40					45				
atc	atg	cct	ggc	tta	tca	ccc	aat	gca	cat	gcc	gca	cac	cat	gac	agc	192
Ile	Met	Pro	Gly	Leu	Ser	Pro	Asn	Ala	His	Ala	Ala	His	His	Asp	Ser	
	50					55					60					
aat	gct	gag	cca	ggc	tgg	tgg	gag	tca	atg	cta	ggt	cca	ggc	aaa	ccc	240
Asn	Ala	Glu	Pro	Gly	Trp	Trp	Glu	Ser	Met	Leu	Gly	Pro	Gly	Lys	Pro	
65					70					75					80	
atc	gac	aca	gac	cgt	tgg	ttc	gtg	atc	tgt	gtc	aac	tca	ctt	ggt	agc	288
Ile	Asp	Thr	Asp	Arg	Trp	Phe	Val	Ile	Cys	Val	Asn	Ser	Leu	Gly	Ser	
				85					90					95		
tgc	aaa	gga	tcg	act	ggc	cct	gca	tcg	tac	aac	ccc	atc	acg	cag	gcc	336
Cys	Lys	Gly	Ser	Thr	Gly	Pro	Ala	Ser	Tyr	Asn	Pro	Ile	Thr	Gln	Ala	
			100					105					110			
atg	tat	cgt	ttg	gac	ttt	cca	gca	ctg	tca	atc	gaa	gac	ggg	gcc	aac	384
Met	Tyr	Arg	Leu	Asp	Phe	Pro	Ala	Leu	Ser	Ile	Glu	Asp	Gly	Ala	Asn	
		115					120					125				
gcc	gca	att	gaa	gtg	gta	cat	gca	ctg	ggc	atc	aag	caa	ctt	gcc	agc	432
Ala	Ala	Ile	Glu	Val	Val	His	Ala	Leu	Gly	Ile	Lys	Gln	Leu	Ala	Ser	
	130					135					140					
ctg	atc	ggc	aat	tca	atg	ggg	ggc	atg	acg	aca	ctg	gcc	atc	ctg	ctg	480
Leu	Ile	Gly	Asn	Ser	Met	Gly	Gly	Met	Thr	Thr	Leu	Ala	Ile	Leu	Leu	
145					150					155					160	
tta	cat	cca	gat	att	gcc	cgc	agc	cac	atc	aac	atc	tca	ggc	agc	gcg	528
Leu	His	Pro	Asp	Ile	Ala	Arg	Ser	His	Ile	Asn	Ile	Ser	Gly	Ser	Ala	
				165					170					175		
cag	gca	tta	ccg	ttt	tcc	atc	gcc	att	cgc	tcg	cta	caa	cgc	gag	gcg	576
Gln	Ala	Leu	Pro	Phe	Ser	Ile	Ala	Ile	Arg	Ser	Leu	Gln	Arg	Glu	Ala	
			180					185					190			
atc	cgc	ctg	gac	ccc	cat	tgg	aag	cag	gga	gac	tac	gac	gac	acc	cac	624
Ile	Arg	Leu	Asp	Pro	His	Trp	Lys	Gln	Gly	Asp	Tyr	Asp	Asp	Thr	His	
		195					200					205				
tac	ccg	gaa	tcg	ggg	cta	cgc	atc	gca	cgc	aaa	ctc	ggg	gtg	atc	acc	672
Tyr	Pro	Glu	Ser	Gly	Leu	Arg	Ile	Ala	Arg	Lys	Leu	Gly	Val	Ile	Thr	
	210					215					220					
tac	cgc	tcc	gcg	ctg	gaa	tgg	gac	ggg	cgt	ttt	ggc	cgg	gta	cgc	ttg	720
Tyr	Arg	Ser	Ala	Leu	Glu	Trp	Asp	Gly	Arg	Phe	Gly	Arg	Val	Arg	Leu	
225					230					235					240	
gat	tcg	gac	caa	acc	aac	gac	aca	cca	ttc	gga	ctg	gaa	ttc	caa	att	768
Asp	Ser	Asp	Gln	Thr	Asn	Asp	Thr	Pro	Phe	Gly	Leu	Glu	Phe	Gln	Ile	
				245					250					255		
gaa	aac	tac	ttg	gaa	agc	cat	gca	cac	cgc	ttc	gtg	cac	acc	ttc	gac	816
Glu	Asn	Tyr	Leu	Glu	Ser	His	Ala	His	Arg	Phe	Val	His	Thr	Phe	Asp	
			260					265					270			
cca	aac	tgc	tac	ctg	tac	ctg	agc	cgc	tcc	atg	gac	tgg	ttc	gac	gtg	864
Pro	Asn	Cys	Tyr	Leu	Tyr	Leu	Ser	Arg	Ser	Met	Asp	Trp	Phe	Asp	Val	

275	280	285	
gcc gag tac gcc aat gga gac att ctt gcc ggg ctg gcc agg atc cga Ala Glu Tyr Ala Asn Gly Asp Ile Leu Ala Gly Leu Ala Arg Ile Arg 290 295 300			912
atc caa cgc gca ctt gcc atc ggt agc cat acc gac atc ctc ttt cca Ile Gln Arg Ala Leu Ala Ile Gly Ser His Thr Asp Ile Leu Phe Pro 305 310 315 320			960
ata caa cag caa caa caa att gcc gaa ggg cta cgc cgt ggc ggt aca Ile Gln Gln Gln Gln Gln Ile Ala Glu Gly Leu Arg Arg Gly Gly Thr 325 330 335			1008
cac gcc acc ttc ctg ggc ctt gac tca ccg cag gga cat gat gcg ttc His Ala Thr Phe Leu Gly Leu Asp Ser Pro Gln Gly His Asp Ala Phe 340 345 350			1056
ctt gtg gat atc gca gga ttt ggc cct cca gtg aag gaa ttt ctg ggc Leu Val Asp Ile Ala Gly Phe Gly Pro Pro Val Lys Glu Phe Leu Gly 355 360 365			1104
gaa ctg tga Glu Leu 370			1113

<210> 38
 <211> 370
 <212> PRT
 <213> Xylella oleander

<400> 38
 Met Thr Glu Phe Ile Pro Pro Gly Ser Leu Phe His Ala Leu Ser Ser
 1 5 10 15
 Pro Phe Ala Met Lys Arg Gly Gly Gln Leu His His Ala Arg Ile Ala
 20 25 30
 Tyr Glu Thr Trp Gly Arg Leu Asn Ala Ser Ala Thr Asn Ala Ile Leu
 35 40 45
 Ile Met Pro Gly Leu Ser Pro Asn Ala His Ala Ala His His Asp Ser
 50 55 60
 Asn Ala Glu Pro Gly Trp Trp Glu Ser Met Leu Gly Pro Gly Lys Pro
 65 70 75 80
 Ile Asp Thr Asp Arg Trp Phe Val Ile Cys Val Asn Ser Leu Gly Ser
 85 90 95
 Cys Lys Gly Ser Thr Gly Pro Ala Ser Tyr Asn Pro Ile Thr Gln Ala
 100 105 110
 Met Tyr Arg Leu Asp Phe Pro Ala Leu Ser Ile Glu Asp Gly Ala Asn
 115 120 125
 Ala Ala Ile Glu Val Val His Ala Leu Gly Ile Lys Gln Leu Ala Ser
 130 135 140
 Leu Ile Gly Asn Ser Met Gly Gly Met Thr Thr Leu Ala Ile Leu Leu
 145 150 155 160
 Leu His Pro Asp Ile Ala Arg Ser His Ile Asn Ile Ser Gly Ser Ala
 165 170 175
 Gln Ala Leu Pro Phe Ser Ile Ala Ile Arg Ser Leu Gln Arg Glu Ala

180					185					190					
Ile	Arg	Leu	Asp	Pro	His	Trp	Lys	Gln	Gly	Asp	Tyr	Asp	Asp	Thr	His
	195						200					205			
Tyr	Pro	Glu	Ser	Gly	Leu	Arg	Ile	Ala	Arg	Lys	Leu	Gly	Val	Ile	Thr
	210					215					220				
Tyr	Arg	Ser	Ala	Leu	Glu	Trp	Asp	Gly	Arg	Phe	Gly	Arg	Val	Arg	Leu
	225					230					235				240
Asp	Ser	Asp	Gln	Thr	Asn	Asp	Thr	Pro	Phe	Gly	Leu	Glu	Phe	Gln	Ile
			245						250					255	
Glu	Asn	Tyr	Leu	Glu	Ser	His	Ala	His	Arg	Phe	Val	His	Thr	Phe	Asp
			260					265						270	
Pro	Asn	Cys	Tyr	Leu	Tyr	Leu	Ser	Arg	Ser	Met	Asp	Trp	Phe	Asp	Val
		275					280					285			
Ala	Glu	Tyr	Ala	Asn	Gly	Asp	Ile	Leu	Ala	Gly	Leu	Ala	Arg	Ile	Arg
	290					295					300				
Ile	Gln	Arg	Ala	Leu	Ala	Ile	Gly	Ser	His	Thr	Asp	Ile	Leu	Phe	Pro
	305					310					315				320
Ile	Gln	Gln	Gln	Gln	Gln	Ile	Ala	Glu	Gly	Leu	Arg	Arg	Gly	Gly	Thr
				325					330					335	
His	Ala	Thr	Phe	Leu	Gly	Leu	Asp	Ser	Pro	Gln	Gly	His	Asp	Ala	Phe
			340				345						350		
Leu	Val	Asp	Ile	Ala	Gly	Phe	Gly	Pro	Pro	Val	Lys	Glu	Phe	Leu	Gly
		355					360					365			
Glu	Leu														
	370														

<210> 39
 <211> 1578
 <212> DNA
 <213> Emericella nidulans

<220>
 <221> CDS
 <222> (1)..(1575)
 <223> REN00010

<400> 39																
atg	agt	ccg	ctg	aac	ggc	gtc	gct	cgt	tcc	ttt	ccg	cgg	ccc	ttc	cag	48
Met	Ser	Pro	Leu	Asn	Gly	Val	Ala	Arg	Ser	Phe	Pro	Arg	Pro	Phe	Gln	
1				5				10					15			
gcc	gtg	acc	agg	cgg	cct	ttt	cga	gtt	gtc	cag	ccg	gcc	atc	gcc	tgt	96
Ala	Val	Thr	Arg	Arg	Pro	Phe	Arg	Val	Val	Gln	Pro	Ala	Ile	Ala	Cys	
			20					25					30			
ccg	tcc	aac	agc	cgg	tcg	ttt	aac	cat	tct	cga	tca	tta	cga	tca	acg	144
Pro	Ser	Asn	Ser	Arg	Ser	Phe	Asn	His	Ser	Arg	Ser	Leu	Arg	Ser	Thr	
		35					40					45				
ggg	tct	cag	tcc	ccc	gct	cca	tcc	cca	cgc	gac	tcc	tcg	aat	ccc	gcg	192
Gly	Ser	Gln	Ser	Pro	Ala	Pro	Ser	Pro	Arg	Asp	Ser	Ser	Asn	Pro	Ala	
	50					55				60						
ctg	tcc	ttc	cct	tgc	ctc	gac	gcc	cag	gag	gcc	aag	tcc	gct	ctt	ctt	240

Leu 65	Ser	Phe	Pro	Cys	Leu 70	Asp	Ala	Gln	Glu	Ala 75	Lys	Ser	Ala	Leu	Leu 80	
tcc	gcg	cga	tct	ctt	ggg	tca	ggc	cct	gaa	ccc	tcc	tat	acc	gcc	ggc	288
Ser	Ala	Arg	Ser	Leu	Gly	Ser	Gly	Pro	Glu	Pro	Ser	Tyr	Thr	Ala	Gly	
				85					90					95		
cac	cac	gaa	cga	ttc	cat	tcc	gac	gaa	ccg	ctg	ctc	ctt	gat	tgg	ggc	336
His	His	Glu	Arg	Phe	His	Ser	Asp	Glu	Pro	Leu	Leu	Leu	Asp	Trp	Gly	
			100					105					110			
ggg	ttg	ctt	cca	gaa	ttt	gat	atc	gca	tat	gag	aca	tgg	ggc	cag	ctg	384
Gly	Leu	Leu	Pro	Glu	Phe	Asp	Ile	Ala	Tyr	Glu	Thr	Trp	Gly	Gln	Leu	
		115					120					125				
aac	gag	aag	aag	gat	aat	gtc	att	ctg	ctg	cat	acc	ggg	ctg	tct	gca	432
Asn	Glu	Lys	Lys	Asp	Asn	Val	Ile	Leu	Leu	His	Thr	Gly	Leu	Ser	Ala	
	130					135					140					
tct	agc	cat	gcg	cac	agc	acc	gaa	gcg	aac	ccg	aag	ccc	ggc	tgg	tgg	480
Ser	Ser	His	Ala	His	Ser	Thr	Glu	Ala	Asn	Pro	Lys	Pro	Gly	Trp	Trp	
145					150					155					160	
gag	aaa	ttc	ata	ggg	cct	ggg	aag	acg	cta	gat	acg	gac	aag	tac	ttt	528
Glu	Lys	Phe	Ile	Gly	Pro	Gly	Lys	Thr	Leu	Asp	Thr	Asp	Lys	Tyr	Phe	
				165					170					175		
gtg	atc	tgc	acc	aat	gtc	ctt	gga	ggg	tgc	tac	ggg	agc	acg	ggg	ccc	576
Val	Ile	Cys	Thr	Asn	Val	Leu	Gly	Gly	Cys	Tyr	Gly	Ser	Thr	Gly	Pro	
			180					185					190			
tcg	acg	gtg	gac	ccg	tcg	gat	ggg	aag	aag	tat	gct	acg	cgg	ttt	ccc	624
Ser	Thr	Val	Asp	Pro	Ser	Asp	Gly	Lys	Lys	Tyr	Ala	Thr	Arg	Phe	Pro	
		195					200					205				
atc	ctg	aca	att	gaa	gat	atg	gtg	cga	gcg	cag	ttc	cgc	ctt	ttg	gac	672
Ile	Leu	Thr	Ile	Glu	Asp	Met	Val	Arg	Ala	Gln	Phe	Arg	Leu	Leu	Asp	
		210				215					220					
cat	ctt	ggg	gtt	cgg	aaa	ctc	tac	gcg	tcc	gtc	ggc	tcc	agc	atg	ggg	720
His	Leu	Gly	Val	Arg	Lys	Leu	Tyr	Ala	Ser	Val	Gly	Ser	Ser	Met	Gly	
225					230					235					240	
ggg	atg	cag	agt	ctt	gca	gcc	ggg	gtt	ctg	ttc	cca	gag	cga	gtg	ggc	768
Gly	Met	Gln	Ser	Leu	Ala	Ala	Gly	Val	Leu	Phe	Pro	Glu	Arg	Val	Gly	
				245					250					255		
aag	att	gtg	tcg	att	agc	ggg	tgt	gct	cga	agc	cat	ccg	tac	agc	att	816
Lys	Ile	Val	Ser	Ile	Ser	Gly	Cys	Ala	Arg	Ser	His	Pro	Tyr	Ser	Ile	
			260					265					270			
gct	atg	cgc	cat	acc	cag	cgg	cag	gtg	ttg	atg	atg	gat	cca	aat	tgg	864
Ala	Met	Arg	His	Thr	Gln	Arg	Gln	Val	Leu	Met	Met	Asp	Pro	Asn	Trp	
		275					280					285				
gct	cga	ggg	ttc	tac	tac	gat	tcg	atc	cca	cct	cat	tca	ggc	atg	aag	912
Ala	Arg	Gly	Phe	Tyr	Tyr	Asp	Ser	Ile	Pro	Pro	His	Ser	Gly	Met	Lys	
		290				295					300					
ctc	gct	cgc	gag	att	gcc	acc	gtc	acg	tac	cgc	agc	gga	cca	gaa	tgg	960
Leu	Ala	Arg	Glu	Ile	Ala	Thr	Val	Thr	Tyr	Arg	Ser	Gly	Pro	Glu	Trp	
305					310					315					320	
gag	aaa	cgc	ttt	ggg	cgg	aaa	cgg	gct	gat	ccg	agc	aaa	cag	cct	gcg	1008
Glu	Lys	Arg	Phe	Gly	Arg	Lys	Arg	Ala	Asp	Pro	Ser	Lys	Gln	Pro	Ala	
				325					330					335		

ctt tgc ccc gac ttt ctc atc gag acg tat ctc gac cac gcc ggt gaa 1056
 Leu Cys Pro Asp Phe Leu Ile Glu Thr Tyr Leu Asp His Ala Gly Glu
 340 345 350

aaa ttc tgc ttg gaa tac gat gcc aac agc ctg ctc tac atc tcc aag 1104
 Lys Phe Cys Leu Glu Tyr Asp Ala Asn Ser Leu Leu Tyr Ile Ser Lys
 355 360 365

gcg atg gat ctg ttt gac cta ggg ttg act cag caa ctc gcg acg aag 1152
 Ala Met Asp Leu Phe Asp Leu Gly Leu Thr Gln Gln Leu Ala Thr Lys
 370 375 380

aag cag agg gcg gag gcc cag gcg aag att agc agc gga aca aac act 1200
 Lys Gln Arg Ala Glu Ala Gln Ala Lys Ile Ser Ser Gly Thr Asn Thr
 385 390 395 400

gtc aat gat gcg tcg tgc agc ctt aca ctt cct gaa cag cca tac cag 1248
 Val Asn Asp Ala Ser Cys Ser Leu Thr Leu Pro Glu Gln Pro Tyr Gln
 405 410 415

gag cag cca tct gcc tcg aca tcc gcc gag cag tct gct tcc gct tca 1296
 Glu Gln Pro Ser Ala Ser Thr Ser Ala Glu Gln Ser Ala Ser Ala Ser
 420 425 430

gag acc ggg tcg gct ccg aac gat ctt gtt gcc ggg ctt gcg ccg ctg 1344
 Glu Thr Gly Ser Ala Pro Asn Asp Leu Val Ala Gly Leu Ala Pro Leu
 435 440 445

aaa gac cat cag gtg ctg gta atc gga gtc gca agc gac att ctc ttc 1392
 Lys Asp His Gln Val Leu Val Ile Gly Val Ala Ser Asp Ile Leu Phe
 450 455 460

ccg gcg tgg caa cag cgc gag atc gcg gag act ctg att caa gca ggg 1440
 Pro Ala Trp Gln Gln Arg Glu Ile Ala Glu Thr Leu Ile Gln Ala Gly
 465 470 475 480

aac aag acc gtg gag cat att gag ctg ggc aac gac gtg tct ctc ttt 1488
 Asn Lys Thr Val Glu His Ile Glu Leu Gly Asn Asp Val Ser Leu Phe
 485 490 495

ggt cat gac aca ttc ctc ctt gat gtc aga acg tcg gag gcg cag ttc 1536
 Gly His Asp Thr Phe Leu Leu Asp Val Arg Thr Ser Glu Ala Gln Phe
 500 505 510

gca agt tcc gta cta gtc ggc tcg cac ata att gta caa tag 1578
 Ala Ser Ser Val Leu Val Gly Ser His Ile Ile Val Gln
 515 520 525

<210> 40

<211> 525

<212> PRT

<213> Emericella nidulans

<400> 40

Met Ser Pro Leu Asn Gly Val Ala Arg Ser Phe Pro Arg Pro Phe Gln
 1 5 10 15

Ala Val Thr Arg Arg Pro Phe Arg Val Val Gln Pro Ala Ile Ala Cys
 20 25 30

Pro Ser Asn Ser Arg Ser Phe Asn His Ser Arg Ser Leu Arg Ser Thr
 35 40 45

Gly Ser Gln Ser Pro Ala Pro Ser Pro Arg Asp Ser Ser Asn Pro Ala
 50 55 60

Leu Ser Phe Pro Cys Leu Asp Ala Gln Glu Ala Lys Ser Ala Leu Leu
 65 70 75 80
 Ser Ala Arg Ser Leu Gly Ser Gly Pro Glu Pro Ser Tyr Thr Ala Gly
 85 90 95
 His His Glu Arg Phe His Ser Asp Glu Pro Leu Leu Leu Asp Trp Gly
 100 105 110
 Gly Leu Leu Pro Glu Phe Asp Ile Ala Tyr Glu Thr Trp Gly Gln Leu
 115 120 125
 Asn Glu Lys Lys Asp Asn Val Ile Leu Leu His Thr Gly Leu Ser Ala
 130 135 140
 Ser Ser His Ala His Ser Thr Glu Ala Asn Pro Lys Pro Gly Trp Trp
 145 150 155 160
 Glu Lys Phe Ile Gly Pro Gly Lys Thr Leu Asp Thr Asp Lys Tyr Phe
 165 170 175
 Val Ile Cys Thr Asn Val Leu Gly Gly Cys Tyr Gly Ser Thr Gly Pro
 180 185 190
 Ser Thr Val Asp Pro Ser Asp Gly Lys Lys Tyr Ala Thr Arg Phe Pro
 195 200 205
 Ile Leu Thr Ile Glu Asp Met Val Arg Ala Gln Phe Arg Leu Leu Asp
 210 215 220
 His Leu Gly Val Arg Lys Leu Tyr Ala Ser Val Gly Ser Ser Met Gly
 225 230 235 240
 Gly Met Gln Ser Leu Ala Ala Gly Val Leu Phe Pro Glu Arg Val Gly
 245 250 255
 Lys Ile Val Ser Ile Ser Gly Cys Ala Arg Ser His Pro Tyr Ser Ile
 260 265 270
 Ala Met Arg His Thr Gln Arg Gln Val Leu Met Met Asp Pro Asn Trp
 275 280 285
 Ala Arg Gly Phe Tyr Tyr Asp Ser Ile Pro Pro His Ser Gly Met Lys
 290 295 300
 Leu Ala Arg Glu Ile Ala Thr Val Thr Tyr Arg Ser Gly Pro Glu Trp
 305 310 315 320
 Glu Lys Arg Phe Gly Arg Lys Arg Ala Asp Pro Ser Lys Gln Pro Ala
 325 330 335
 Leu Cys Pro Asp Phe Leu Ile Glu Thr Tyr Leu Asp His Ala Gly Glu
 340 345 350
 Lys Phe Cys Leu Glu Tyr Asp Ala Asn Ser Leu Leu Tyr Ile Ser Lys
 355 360 365
 Ala Met Asp Leu Phe Asp Leu Gly Leu Thr Gln Gln Leu Ala Thr Lys
 370 375 380
 Lys Gln Arg Ala Glu Ala Gln Ala Lys Ile Ser Ser Gly Thr Asn Thr
 385 390 395 400
 Val Asn Asp Ala Ser Cys Ser Leu Thr Leu Pro Glu Gln Pro Tyr Gln
 405 410 415
 Glu Gln Pro Ser Ala Ser Thr Ser Ala Glu Gln Ser Ala Ser Ala Ser

420	425	430
Glu Thr Gly Ser Ala Pro Asn Asp Leu Val Ala Gly Leu Ala Pro Leu		
435	440	445
Lys Asp His Gln Val Leu Val Ile Gly Val Ala Ser Asp Ile Leu Phe		
450	455	460
Pro Ala Trp Gln Gln Arg Glu Ile Ala Glu Thr Leu Ile Gln Ala Gly		
465	470	475
Asn Lys Thr Val Glu His Ile Glu Leu Gly Asn Asp Val Ser Leu Phe		
485	490	495
Gly His Asp Thr Phe Leu Leu Asp Val Arg Thr Ser Glu Ala Gln Phe		
500	505	510
Ala Ser Ser Val Leu Val Gly Ser His Ile Ile Val Gln		
515	520	525

<210> 41
 <211> 1170
 <212> DNA
 <213> Mesorhizobium loti

 <220>
 <221> CDS
 <222> (1)..(1167)
 <223> NP_104621

<400> 41
 atg gcc gct ctg cgc gca gga aag acc aac aac gag gcc gac cag ccg 48
 Met Ala Ala Leu Arg Ala Gly Lys Thr Asn Asn Glu Ala Asp Gln Pro
 1 5 10 15

 tcg agc ccg gtg ttg cgc ttc ggg gcg gac aag ccg ctc aag ctc gac 96
 Ser Ser Pro Val Leu Arg Phe Gly Ala Asp Lys Pro Leu Lys Leu Asp
 20 25 30

 gcc ggc acg ctt ttg tgc ccg ttc cag atc gcc tat cag acc tac ggc 144
 Ala Gly Thr Leu Leu Ser Pro Phe Gln Ile Ala Tyr Gln Thr Tyr Gly
 35 40 45

 acg ctg aac gat gcc cgc tcc aat gcc atc ctc gtc tgc cat gcg ctg 192
 Thr Leu Asn Asp Ala Arg Ser Asn Ala Ile Leu Val Cys His Ala Leu
 50 55 60

 acc ggc gac cag cat gtc gcc aac acc aat ccg gtg acc ggc aag ccg 240
 Thr Gly Asp Gln His Val Ala Asn Thr Asn Pro Val Thr Gly Lys Pro
 65 70 75 80

 gga tgg tgg gaa gtg ctg atc ggc ccc ggc agg atc atc gac acc aac 288
 Gly Trp Trp Glu Val Leu Ile Gly Pro Gly Arg Ile Ile Asp Thr Asn
 85 90 95

 cgt ttc ttc gtc atc tgc tcc aac gtc atc ggc ggt tgt ctg ggc tcc 336
 Arg Phe Phe Val Ile Cys Ser Asn Val Ile Gly Gly Cys Leu Gly Ser
 100 105 110

 acc ggc ccg gcc tgc acc aac ccc gcc acc ggc aag ccc tac ggg ctc 384
 Thr Gly Pro Ala Ser Thr Asn Pro Ala Thr Gly Lys Pro Tyr Gly Leu
 115 120 125

 gac ctg ccg gtc atc acc atc cgc gat atg gtg cgc gcg cag cag atg 432
 Asp Leu Pro Val Ile Thr Ile Arg Asp Met Val Arg Ala Gln Gln Met
 130 135 140

ctg atc gat cat ttc ggc atc gag aaa ctg ttc tgc gtg ctc ggc ggc Leu Ile Asp His Phe Gly Ile Glu Lys Leu Phe Cys Val Leu Gly Gly 145 150 155 160	480
tgc atg ggc gga atg cag gtg ctg gaa tgg gcg tgc agc tac ccc gag Ser Met Gly Gly Met Gln Val Leu Glu Trp Ala Ser Ser Tyr Pro Glu 165 170 175	528
cgc gtc ttt tgc gca ctg ccg atc gcc acc ggc gcg cgc cat tcc tgc Arg Val Phe Ser Ala Leu Pro Ile Ala Thr Gly Ala Arg His Ser Ser 180 185 190	576
cag aac atc gcc ttc cac gag gtc ggc cgg cag gct gtc atg gcc gat Gln Asn Ile Ala Phe His Glu Val Gly Arg Gln Ala Val Met Ala Asp 195 200 205	624
ccg gac tgg cac ggc ggc aaa tat ttc gaa aac ggc aaa cgc ccg gaa Pro Asp Trp His Gly Gly Lys Tyr Phe Glu Asn Gly Lys Arg Pro Glu 210 215 220	672
aag ggc ctg gcg gta gcg cgc atg gcc gcc cac ata acc tat ctg tgc Lys Gly Leu Ala Val Ala Arg Met Ala Ala His Ile Thr Tyr Leu Ser 225 230 235 240	720
gaa gcc gcc ctg cac cgg aaa ttc ggc cgc aat ctg cag gat cgc gag Glu Ala Ala Leu His Arg Lys Phe Gly Arg Asn Leu Gln Asp Arg Glu 245 250 255	768
gcg ctg acc ttc ggc ttc gac gcc gac ttc cag atc gaa agc tat ctg Ala Leu Thr Phe Gly Phe Asp Ala Asp Phe Gln Ile Glu Ser Tyr Leu 260 265 270	816
cgc cac caa ggc atg acc ttc gtc gac cgc ttc gac gcc aat tcc tat Arg His Gln Gly Met Thr Phe Val Asp Arg Phe Asp Ala Asn Ser Tyr 275 280 285	864
ctc tac atg acg cgg tgc atg gac tat ttc gac ctc gcc gcc gat cat Leu Tyr Met Thr Arg Ser Met Asp Tyr Phe Asp Leu Ala Ala Asp His 290 295 300	912
ggc ggg cgg ctg gcg gat gcc ttt gcc ggc acc aaa acc cgc ttc tgc Gly Gly Arg Leu Ala Asp Ala Phe Ala Gly Thr Lys Thr Arg Phe Cys 305 310 315 320	960
ctg gtg tcc ttc acc tgc gat tgg ttg ttt ccg acc gaa gag agc cgc Leu Val Ser Phe Thr Ser Asp Trp Leu Phe Pro Thr Glu Glu Ser Arg 325 330 335	1008
tgc atc gtg cac gcg ctc aac gcc gcc ggc gcg tcc gtg tcc ttc gtc Ser Ile Val His Ala Leu Asn Ala Ala Gly Ala Ser Val Ser Phe Val 340 345 350	1056
gaa atc gag acc gac cgc ggc cac gat gcc ttc ctg ctc gac gag ccg Glu Ile Glu Thr Asp Arg Gly His Asp Ala Phe Leu Leu Asp Glu Pro 355 360 365	1104
gaa ctg ttc gcc gcc atc aac ggc ttc atc ggc tcc gcg gcg cgg gcg Glu Leu Phe Ala Ala Ile Asn Gly Phe Ile Gly Ser Ala Ala Arg Ala 370 375 380	1152
aga ggg cta agc gca tga Arg Gly Leu Ser Ala 385	1170

<210> 42

<211> 389

<212> PRT

<213> Mesorhizobium loti

<400> 42

Met Ala Ala Leu Arg Ala Gly Lys Thr Asn Asn Glu Ala Asp Gln Pro
 1 5 10 15

Ser Ser Pro Val Leu Arg Phe Gly Ala Asp Lys Pro Leu Lys Leu Asp
 20 25 30

Ala Gly Thr Leu Leu Ser Pro Phe Gln Ile Ala Tyr Gln Thr Tyr Gly
 35 40 45

Thr Leu Asn Asp Ala Arg Ser Asn Ala Ile Leu Val Cys His Ala Leu
 50 55 60

Thr Gly Asp Gln His Val Ala Asn Thr Asn Pro Val Thr Gly Lys Pro
 65 70 75 80

Gly Trp Trp Glu Val Leu Ile Gly Pro Gly Arg Ile Ile Asp Thr Asn
 85 90 95

Arg Phe Phe Val Ile Cys Ser Asn Val Ile Gly Gly Cys Leu Gly Ser
 100 105 110

Thr Gly Pro Ala Ser Thr Asn Pro Ala Thr Gly Lys Pro Tyr Gly Leu
 115 120 125

Asp Leu Pro Val Ile Thr Ile Arg Asp Met Val Arg Ala Gln Gln Met
 130 135 140

Leu Ile Asp His Phe Gly Ile Glu Lys Leu Phe Cys Val Leu Gly Gly
 145 150 155 160

Ser Met Gly Gly Met Gln Val Leu Glu Trp Ala Ser Ser Tyr Pro Glu
 165 170 175

Arg Val Phe Ser Ala Leu Pro Ile Ala Thr Gly Ala Arg His Ser Ser
 180 185 190

Gln Asn Ile Ala Phe His Glu Val Gly Arg Gln Ala Val Met Ala Asp
 195 200 205

Pro Asp Trp His Gly Gly Lys Tyr Phe Glu Asn Gly Lys Arg Pro Glu
 210 215 220

Lys Gly Leu Ala Val Ala Arg Met Ala Ala His Ile Thr Tyr Leu Ser
 225 230 235 240

Glu Ala Ala Leu His Arg Lys Phe Gly Arg Asn Leu Gln Asp Arg Glu
 245 250 255

Ala Leu Thr Phe Gly Phe Asp Ala Asp Phe Gln Ile Glu Ser Tyr Leu
 260 265 270

Arg His Gln Gly Met Thr Phe Val Asp Arg Phe Asp Ala Asn Ser Tyr
 275 280 285

Leu Tyr Met Thr Arg Ser Met Asp Tyr Phe Asp Leu Ala Ala Asp His
 290 295 300

Gly Gly Arg Leu Ala Asp Ala Phe Ala Gly Thr Lys Thr Arg Phe Cys
 305 310 315 320

Leu Val Ser Phe Thr Ser Asp Trp Leu Phe Pro Thr Glu Glu Ser Arg
 325 330 335

Ser Ile Val His Ala Leu Asn Ala Ala Gly Ala Ser Val Ser Phe Val
340 345 350

Glu Ile Glu Thr Asp Arg Gly His Asp Ala Phe Leu Leu Asp Glu Pro
355 360 365

Glu Leu Phe Ala Ala Ile Asn Gly Phe Ile Gly Ser Ala Ala Arg Ala
370 375 380

Arg Gly Leu Ser Ala
385

<210> 43

<211> 1155

<212> DNA

<213> acremonium crysogenum

<220>

<221> CDS

<222> (1)..(1152)

<223> P39058

<400> 43

tgt	cgc	ctc	aga	tcg	cca	atc	gct	tcg	agg	ctt	cgc	tag	atg	ccc	aag	48
Cys	Arg	Leu	Arg	Ser	Pro	Ile	Ala	Ser	Arg	Leu	Arg	Xaa	Met	Pro	Lys	
1				5					10					15		

aca	tag	cca	gaa	tat	cgc	tct	tca	cac	tgg	aat	ctg	gcg	tca	tcc	ttc	96
Thr	Xaa	Pro	Glu	Tyr	Arg	Ser	Ser	His	Trp	Asn	Leu	Ala	Ser	Ser	Phe	
			20					25					30			

gcg	atg	tac	ccg	tgg	cat	aca	aat	cgt	ggg	gtc	gca	tga	atg	tct	caa	144
Ala	Met	Tyr	Pro	Trp	His	Thr	Asn	Arg	Gly	Val	Ala	Xaa	Met	Ser	Gln	
		35					40					45				

ggg	ata	act	gcg	tca	tcg	tct	gcc	aca	cct	tga	cga	gca	gcg	ccc	atg	192
Gly	Ile	Thr	Ala	Ser	Ser	Ser	Ala	Thr	Pro	Xaa	Arg	Ala	Ala	Pro	Met	
	50					55					60					

tca	cct	cgt	ggt	ggc	cca	cac	tgt	ttg	gcc	aag	gca	ggg	ctt	tcg	ata	240
Ser	Pro	Arg	Gly	Gly	Pro	His	Cys	Leu	Ala	Lys	Ala	Gly	Leu	Ser	Ile	
65					70					75					80	

cct	ctc	gct	act	tca	tca	tct	gcc	taa	att	atc	tcg	gga	gcc	cct	ttg	288
Pro	Leu	Ala	Thr	Ser	Ser	Ser	Ala	Xaa	Ile	Ile	Ser	Gly	Ala	Pro	Leu	
				85					90					95		

gga	gtg	ctg	gac	cat	gtt	cac	cgg	acc	ccg	atg	cag	aag	gcc	agc	gcc	336
Gly	Val	Leu	Asp	His	Val	His	Arg	Thr	Pro	Met	Gln	Lys	Ala	Ser	Ala	
			100					105					110			

cgt	acg	ggg	cca	agt	ttc	ctc	gca	cga	cga	ttc	gag	atg	atg	ttc	gta	384
Arg	Thr	Gly	Pro	Ser	Phe	Leu	Ala	Arg	Arg	Phe	Glu	Met	Met	Phe	Val	
		115					120					125				

ttc	atc	gcc	agg	tgc	tcg	aca	ggt	tag	gcg	tca	ggc	aaa	ttg	ctg	ccg	432
Phe	Ile	Ala	Arg	Cys	Ser	Thr	Gly	Xaa	Ala	Ser	Gly	Lys	Leu	Leu	Pro	
	130					135					140					

tag	tcg	gcg	cat	cca	tgg	gtg	gaa	tgc	aca	ctc	tgg	aat	ggg	cct	tct	480
Xaa	Ser	Ala	His	Pro	Trp	Val	Glu	Cys	Thr	Leu	Trp	Asn	Gly	Pro	Ser	
145					150					155					160	

ttg	gtc	ccg	agt	acg	tgc	gaa	aga	ttg	tgc	cca	tcg	cga	cat	cat	gcc	528
Leu	Val	Pro	Ser	Thr	Cys	Glu	Arg	Leu	Cys	Pro	Ser	Arg	His	His	Ala	

165										170					175					
gtc	aga	gcg	gct	ggg	gag	cag	ctt	ggg	tcg	aga	cac	aga	ggc	agt	gca	576				
Val	Arg	Ala	Ala	Gly	Ala	Gln	Leu	Gly	Ser	Arg	His	Arg	Gly	Ser	Ala					
			180					185					190							
tct	atg	atg	acc	cca	agt	acc	tgg	acg	ggg	agt	acg	acg	tag	acg	acc	624				
Ser	Met	Met	Thr	Pro	Ser	Thr	Trp	Thr	Gly	Ser	Thr	Thr	Xaa	Thr	Thr					
		195					200					205								
agc	ctg	tcc	ggg	ggc	tcg	aaa	cag	cgc	gca	aga	ttg	cga	atc	tca	cgt	672				
Ser	Leu	Ser	Gly	Gly	Ser	Lys	Gln	Arg	Ala	Arg	Leu	Arg	Ile	Ser	Arg					
	210					215					220									
aca	aga	gca	aac	ctg	cga	tgg	acg	agc	gct	tcc	ata	tgg	ctc	cag	gag	720				
Thr	Arg	Ala	Asn	Leu	Arg	Trp	Thr	Ser	Ala	Ser	Ile	Trp	Leu	Gln	Glu					
	225				230					235					240					
tcc	aag	ccg	gcc	gga	ata	tca	gca	gcc	agg	atg	cga	aga	agg	aaa	tca	768				
Ser	Lys	Pro	Ala	Gly	Ile	Ser	Ala	Ala	Arg	Met	Arg	Arg	Arg	Lys	Ser					
			245						250					255						
acg	gca	cag	aca	gcg	gca	aca	gcc	acc	gtg	ctg	gcc	agc	cca	ttg	aag	816				
Thr	Ala	Gln	Thr	Ala	Ala	Thr	Ala	Thr	Val	Leu	Ala	Ser	Pro	Leu	Lys					
			260					265					270							
ccg	tat	ctt	cct	atc	tcc	ggg	acc	agg	ccc	aga	agt	ttg	ccg	cga	gct	864				
Pro	Tyr	Leu	Pro	Ile	Ser	Gly	Thr	Arg	Pro	Arg	Ser	Leu	Pro	Arg	Ala					
		275					280					285								
tcg	acg	cca	act	gct	aca	tcg	cca	tga	cac	tca	agt	tcg	aca	ccc	acg	912				
Ser	Thr	Pro	Thr	Ala	Thr		Pro	Xaa	His	Ser	Ser	Ser	Thr	Pro	Thr					
	290					295					300									
aca	tca	gca	gag	gcc	ggg	cag	gat	caa	tcc	cgg	agg	ctc	tgg	caa	tga	960				
Thr	Ser	Ala	Glu	Ala	Gly	Gln	Asp	Gln	Ser	Arg	Arg	Leu	Trp	Gln	Xaa					
	305				310					315					320					
tta	cac	aac	cag	cgt	tga	tca	ttt	gcg	cca	ggg	cag	acg	gtc	tgt	act	1008				
Leu	His	Asn	Gln	Arg	Xaa	Ser	Phe	Ala	Pro	Gly	Gln	Thr	Val	Cys	Thr					
			325						330					335						
cgt	ttg	acg	agc	acg	ttg	aga	tgg	ggc	gca	gta	tcc	caa	aca	gtc	gtc	1056				
Arg	Leu	Thr	Ser	Thr	Leu	Arg	Trp	Gly	Ala	Val	Ser	Gln	Thr	Val	Val					
			340					345					350							
ttt	gcg	tgg	tgg	aca	cga	atg	agg	gtc	atg	act	tct	ttg	taa	tgg	aag	1104				
Phe	Ala	Trp	Trp	Thr	Arg	Met	Arg	Val	Met	Thr	Ser	Leu	Xaa	Trp	Lys					
		355					360					365								
cgg	aca	agg	tta	atg	atg	ccg	tca	gag	gat	tcc	tcg	atc	agt	cat	taa	1152				
Arg	Thr	Arg	Leu	Met	Met	Pro	Ser	Glu	Asp	Ser	Ser	Ile	Ser	His	Xaa					
	370					375					380									
tgt																1155				

<210> 44

<211> 384

<212> PRT

<213> acremonium crysogenum

<220>

<221> unsure

<222> 13 .. 13

<223> All occurrences of Xaa indicate any amino acid

<220>
 <221> unsure
 <222> 18 .. 18
 <223> All occurrences of Xaa indicate any amino acid

<220>
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 <222> 45 .. 45
 <223> All occurrences of Xaa indicate any amino acid

<220>
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 <222> 59 .. 59
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 <222> 89 .. 89
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 <222> 137 .. 137
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<220>
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 <222> 145 .. 145
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<220>
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 <222> 206 .. 206
 <223> All occurrences of Xaa indicate any amino acid

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 <222> 326 .. 326
 <223> All occurrences of Xaa indicate any amino acid

<220>
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 <222> 366 .. 366
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<220>
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 <222> 384 .. 384
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 Thr Xaa Pro Glu Tyr Arg Ser Ser His Trp Asn Leu Ala Ser Ser Phe
 20 25 30

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		35					40					45			
Gly	Ile	Thr	Ala	Ser	Ser	Ser	Ala	Thr	Pro	Xaa	Arg	Ala	Ala	Pro	Met
	50					55					60				
Ser	Pro	Arg	Gly	Gly	Pro	His	Cys	Leu	Ala	Lys	Ala	Gly	Leu	Ser	Ile
65					70					75					80
Pro	Leu	Ala	Thr	Ser	Ser	Ser	Ala	Xaa	Ile	Ile	Ser	Gly	Ala	Pro	Leu
				85					90					95	
Gly	Val	Leu	Asp	His	Val	His	Arg	Thr	Pro	Met	Gln	Lys	Ala	Ser	Ala
			100					105					110		
Arg	Thr	Gly	Pro	Ser	Phe	Leu	Ala	Arg	Arg	Phe	Glu	Met	Met	Phe	Val
		115					120					125			
Phe	Ile	Ala	Arg	Cys	Ser	Thr	Gly	Xaa	Ala	Ser	Gly	Lys	Leu	Leu	Pro
	130					135					140				
Xaa	Ser	Ala	His	Pro	Trp	Val	Glu	Cys	Thr	Leu	Trp	Asn	Gly	Pro	Ser
145					150					155					160
Leu	Val	Pro	Ser	Thr	Cys	Glu	Arg	Leu	Cys	Pro	Ser	Arg	His	His	Ala
				165					170					175	
Val	Arg	Ala	Ala	Gly	Ala	Gln	Leu	Gly	Ser	Arg	His	Arg	Gly	Ser	Ala
			180					185					190		
Ser	Met	Met	Thr	Pro	Ser	Thr	Trp	Thr	Gly	Ser	Thr	Thr	Xaa	Thr	Thr
		195					200					205			
Ser	Leu	Ser	Gly	Gly	Ser	Lys	Gln	Arg	Ala	Arg	Leu	Arg	Ile	Ser	Arg
	210					215					220				
Thr	Arg	Ala	Asn	Leu	Arg	Trp	Thr	Ser	Ala	Ser	Ile	Trp	Leu	Gln	Glu
225					230					235					240
Ser	Lys	Pro	Ala	Gly	Ile	Ser	Ala	Ala	Arg	Met	Arg	Arg	Arg	Lys	Ser
				245					250					255	
Thr	Ala	Gln	Thr	Ala	Ala	Thr	Ala	Thr	Val	Leu	Ala	Ser	Pro	Leu	Lys
			260					265					270		
Pro	Tyr	Leu	Pro	Ile	Ser	Gly	Thr	Arg	Pro	Arg	Ser	Leu	Pro	Arg	Ala
		275					280					285			
Ser	Thr	Pro	Thr	Ala	Thr	Ser	Pro	Xaa	His	Ser	Ser	Ser	Thr	Pro	Thr
	290					295					300				
Thr	Ser	Ala	Glu	Ala	Gly	Gln	Asp	Gln	Ser	Arg	Arg	Leu	Trp	Gln	Xaa
305					310					315					320
Leu	His	Asn	Gln	Arg	Xaa	Ser	Phe	Ala	Pro	Gly	Gln	Thr	Val	Cys	Thr
				325					330					335	
Arg	Leu	Thr	Ser	Thr	Leu	Arg	Trp	Gly	Ala	Val	Ser	Gln	Thr	Val	Val
			340					345					350		
Phe	Ala	Trp	Trp	Thr	Arg	Met	Arg	Val	Met	Thr	Ser	Leu	Xaa	Trp	Lys
		355					360					365			
Arg	Thr	Arg	Leu	Met	Met	Pro	Ser	Glu	Asp	Ser	Ser	Ile	Ser	His	Xaa
	370					375					380				

<210> 45
 <211> 1077
 <212> DNA
 <213> *Pseudomonas putida*

<220>
 <221> CDS
 <222> (1)..(1074)
 <223> AAK49778

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acc tcc cgg ttc gat gaa ccg ctg gca ctg gcc tgt ggc cgt tca ctg 96
 Thr Ser Arg Phe Asp Glu Pro Leu Ala Leu Ala Cys Gly Arg Ser Leu
 20 25 30

gcc agt tac gaa ctg gtc tac gag acc tat ggc acc ctg aac gcc agc 144
 Ala Ser Tyr Glu Leu Val Tyr Glu Thr Tyr Gly Thr Leu Asn Ala Ser
 35 40 45

gcg agc aac gcc gtg ctg atc tgc cat gcc ctg tcc ggc cac cac cat 192
 Ala Ser Asn Ala Val Leu Ile Cys His Ala Leu Ser Gly His His His
 50 55 60

gcc gct ggc tac cat gcc gcc acc gac cgc aag ccg ggc tgg tgg gac 240
 Ala Ala Gly Tyr His Ala Ala Thr Asp Arg Lys Pro Gly Trp Trp Asp
 65 70 75 80

agc tgc atc ggc ccc gga aaa ccg atc gat acc aac cgc ttc ttc gtg 288
 Ser Cys Ile Gly Pro Gly Lys Pro Ile Asp Thr Asn Arg Phe Phe Val
 85 90 95

gtc agc ctg aac aac ctc ggc ggc tgc aac ggc agc acc ggc ccc agc 336
 Val Ser Leu Asn Asn Leu Gly Gly Cys Asn Gly Ser Thr Gly Pro Ser
 100 105 110

agt gtc aac cca gcc acc ggt aaa ccc tat ggc gcc gag ttc ccg gta 384
 Ser Val Asn Pro Ala Thr Gly Lys Pro Tyr Gly Ala Glu Phe Pro Val
 115 120 125

ttg acc gtg gaa gac tgg gtg cac agc cag gca cgg ctg gcc gac cgc 432
 Leu Thr Val Glu Asp Trp Val His Ser Gln Ala Arg Leu Ala Asp Arg
 130 135 140

ctg ggc atc cag cag tgg gca gct atc gtc ggc ggt agc ctg ggt ggc 480
 Leu Gly Ile Gln Gln Trp Ala Ala Ile Val Gly Gly Ser Leu Gly Gly
 145 150 155 160

atg cag gcg ctg caa tgg acg atg acc tac ccc gag cgc gta cgc cac 528
 Met Gln Ala Leu Gln Trp Thr Met Thr Tyr Pro Glu Arg Val Arg His
 165 170 175

tgc gtc gac att gcc tcg gcc ccc aag ctg tcg gcg cag aac atc gcc 576
 Cys Val Asp Ile Ala Ser Ala Pro Lys Leu Ser Ala Gln Asn Ile Ala
 180 185 190

ttc aac gag gtg gcg cgt cag gcc att ctt acc gac cct gag tac cgc 624
 Phe Asn Glu Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Glu Tyr Arg
 195 200 205

aga ggc tcg ttt cca gga cca ggt gtg atc ccc aag cgc ggc ctg atg 672

Arg Gly Ser Phe Pro Gly Pro Gly Val Ile Pro Lys Arg Gly Leu Met
 210 215 220
 ctg gca cgg atg gtc ggc cac att acc tat ctg tcc gat gat tcg atg 720
 Leu Ala Arg Met Val Gly His Ile Thr Tyr Leu Ser Asp Asp Ser Met
 225 230 235 240
 ggt gaa aaa ttc ggc cga gag ctg aaa gcg aca agc tca act acg act 768
 Gly Glu Lys Phe Gly Arg Glu Leu Lys Ala Thr Ser Ser Thr Thr Thr
 245 250 255
 tcc aca gcg tcg agt tcc agg tcg aaa gct acc tgc gct atc agg gcg 816
 Ser Thr Ala Ser Ser Ser Arg Ser Lys Ala Thr Cys Ala Ile Arg Ala
 260 265 270
 agg agt ttt ccg gcc gtt tcg acg cca aca cct acc ttg atg acc aag 864
 Arg Ser Phe Pro Ala Val Ser Thr Pro Thr Pro Thr Leu Met Thr Lys
 275 280 285
 gca ctg gac tat ttc gac ccg gcc gcc acg cac ggt ggt gat ctg gcc 912
 Ala Leu Asp Tyr Phe Asp Pro Ala Ala Thr His Gly Gly Asp Leu Ala
 290 295 300
 gcc acc ctg gcc cac gtc acg gcg gac tac tgc atc tgt cgt tca cca 960
 Ala Thr Leu Ala His Val Thr Ala Asp Tyr Cys Ile Cys Arg Ser Pro
 305 310 315 320
 ccg act gcg ctt ctc tcc ggc ccg ttc gcg cga gat cgt cga cgc gct 1008
 Pro Thr Ala Leu Leu Ser Gly Pro Phe Ala Arg Asp Arg Arg Arg Ala
 325 330 335
 gat ggc cgc gcg caa gaa cgt ctg cta cct gga gat cga ttc gcc cta 1056
 Asp Gly Arg Ala Gln Glu Arg Leu Leu Pro Gly Asp Arg Phe Ala Leu
 340 345 350
 cgg gca cga tgc att tcc tga 1077
 Arg Ala Arg Cys Ile Ser
 355

<210> 46
 <211> 358
 <212> PRT
 <213> Pseudomonas putida

<400> 46
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 Thr Ser Arg Phe Asp Glu Pro Leu Ala Leu Ala Cys Gly Arg Ser Leu
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 Ala Ser Tyr Glu Leu Val Tyr Glu Thr Tyr Gly Thr Leu Asn Ala Ser
 35 40 45
 Ala Ser Asn Ala Val Leu Ile Cys His Ala Leu Ser Gly His His His
 50 55 60
 Ala Ala Gly Tyr His Ala Ala Thr Asp Arg Lys Pro Gly Trp Trp Asp
 65 70 75 80
 Ser Cys Ile Gly Pro Gly Lys Pro Ile Asp Thr Asn Arg Phe Phe Val
 85 90 95
 Val Ser Leu Asn Asn Leu Gly Gly Cys Asn Gly Ser Thr Gly Pro Ser
 100 105 110

Ser Val Asn Pro Ala Thr Gly Lys Pro Tyr Gly Ala Glu Phe Pro Val
 115 120 125
 Leu Thr Val Glu Asp Trp Val His Ser Gln Ala Arg Leu Ala Asp Arg
 130 135 140
 Leu Gly Ile Gln Gln Trp Ala Ala Ile Val Gly Gly Ser Leu Gly Gly
 145 150 155 160
 Met Gln Ala Leu Gln Trp Thr Met Thr Tyr Pro Glu Arg Val Arg His
 165 170 175
 Cys Val Asp Ile Ala Ser Ala Pro Lys Leu Ser Ala Gln Asn Ile Ala
 180 185 190
 Phe Asn Glu Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Glu Tyr Arg
 195 200 205
 Arg Gly Ser Phe Pro Gly Pro Gly Val Ile Pro Lys Arg Gly Leu Met
 210 215 220
 Leu Ala Arg Met Val Gly His Ile Thr Tyr Leu Ser Asp Asp Ser Met
 225 230 235 240
 Gly Glu Lys Phe Gly Arg Glu Leu Lys Ala Thr Ser Ser Thr Thr Thr
 245 250 255
 Ser Thr Ala Ser Ser Ser Arg Ser Lys Ala Thr Cys Ala Ile Arg Ala
 260 265 270
 Arg Ser Phe Pro Ala Val Ser Thr Pro Thr Pro Thr Leu Met Thr Lys
 275 280 285
 Ala Leu Asp Tyr Phe Asp Pro Ala Ala Thr His Gly Gly Asp Leu Ala
 290 295 300
 Ala Thr Leu Ala His Val Thr Ala Asp Tyr Cys Ile Cys Arg Ser Pro
 305 310 315 320
 Pro Thr Ala Leu Leu Ser Gly Pro Phe Ala Arg Asp Arg Arg Arg Ala
 325 330 335
 Asp Gly Arg Ala Gln Glu Arg Leu Leu Pro Gly Asp Arg Phe Ala Leu
 340 345 350
 Arg Ala Arg Cys Ile Ser
 355

<210> 47

<211> 52

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 47

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52

<210> 48

<211> 53

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 48

tctagactcg agcggccgcg gccggccttt aaattgaaga cgaaagggcc tcg 53

<210> 49

<211> 47

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 49

gagatctaga cccggggatc cgctagcggg ctgctaaagg aagcgga 47

<210> 50

<211> 38

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 50

gagagggcgcg ccgctagcgt gggcgaagaa ctccagca 38

<210> 51

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 51

gagagggcgcg ccgcgcaaag tcccgttcg tgaa 34

<210> 52

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 52

gagagggcgcg ccgctcaagt cggcgaagcc acgc 34

<210> 53

<211> 140

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 53

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tcggacctag ggatatcgtc gacatcgatg ctcttctgcg ttaattaaca attgggatcc 120
tctagaccgc ggatttaa 140

<210> 54
 <211> 140
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:PCR primer

<400> 54
 gatcatttaa atccccgggtc tagaggatcc caattgttaa ttaacgcaga agagcatcga 60
 tgtcgacgat atccctaggt ccgaactagt catatgacgc gtggtaccgg gcccgacgtc 120
 aggcctctcg agatttaaataat 140

<210> 55
 <211> 33
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:PCR primer

<400> 55
 gagagcggcc gccgatcctt ttttaacccat cac 33

<210> 56
 <211> 32
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:PCR primer

<400> 56
 aggagcggcc gccatcggca ttttcttttg cg 32

<210> 57
 <211> 5091
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:plasmid

<400> 57
 gccgcgactg ccttcgcgaa gccttgcccc gcggaaattt cctccaccga gttcgtgcac 60
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 tcttcgcaaa aatcgteccc tgatcgccct tgcgacgttg gcgtcgggtg cgctgggtgc 180
 gcttggtctg accgacttga tcagcggccg ctcgatttaa atctcgagag gcctgacgtc 240
 gggccccgta ccacgcgtca tatgactagt tcggacctag ggatatcgtc gacatcgatg 300
 ctcttctgcy ttaattaaca attgggatcc tctagaccog ggatttaaata cgctagcggg 360
 ctgctaaagg aagcgggaaca cgtagaaaagc cagtcgcgag aaacgggtgct gacccccggat 420
 gaatgtcagc tactgggcta tctggacaag ggaaaacgca agcgcaaaga gaaagcaggt 480
 agcttgcaat gggcttacat ggcgatagct agactgggcy gttttatgga cagcaagcga 540
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 gatggctttc ttgccgccaa ggatctgatg gcgcagggga tcaagatctg atcaagagac 660
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 ttgggtggag aggtatttcg gctatgactg ggcacaacag acaatcggct gctctgatgc 780
 cggcgtgttc cggctgtcag cgcaggggcy cccggttctt tttgtcaaga ccgacctgtc 840
 cgggtgccctg aatgaactgc aggacgaggc agcgcggcta tcgtgggtgg ccacgacggg 900
 cgttccttgc gcagctgtgc tcgacgttgt cactgaagcg ggaagggact ggctgctatt 960
 gggcgaagtg ccggggcagg atctcctgtc atctcacctt gctcctgccg agaaagtatc 1020
 catcatggct gatgcaatgc ggcggctgca tacgcttgat ccggctacct gccattcga 1080
 ccaccaagcg aaacatcgca tcgagcgagc acgtactcgg atggaagccg gtcttgtcga 1140

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gaatatcatg	gtggaaaatg	gccgcttttc	tggattcatc	gactgtggcc	ggctgggtgt	1320
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gtatgtaggc	ggtgctacag	agttcttgaa	gtgggtggcct	aactacggct	acactagaag	2340
gacagtatct	ggtagctgcg	ctctgctgaa	gccagttacc	ttcggaaaaa	gagttggtag	2400
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gattacgcgc	agaaaaaaag	gatctcaaga	agatcctttg	atcttttcta	cggggtctga	2520
cgctcagtg	aacgaaaaat	cacgttaagg	gattttgggt	atgagattat	caaaaaggat	2580
cttcacctag	atccttttta	aggccggccg	cggccgcgca	aagtcccgtc	tcgtgaaaat	2640
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<210> 58
 <211> 4323
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: plasmid

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<210> 59
<211> 35
<212> DNA
<213> Artificial sequence

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<220>
<223> Description of the artificial sequence:PCR Primer

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<400> 59
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<210> 60
<211> 34
<212> DNA
<213> Artificial sequence

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<220>
<223> Description of the artificial sequence:PCR Primer

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<400> 60
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<210> 61
<211> 5860
<212> DNA
<213> Artificial sequence

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<220>
<223> Description of the artificial sequence:plasmid

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<210> 62
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<212> DNA
<213> Artificial sequence

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<220>
<223> Description of the artificial sequence:PCR Primer

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<400> 62
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<210> 63
<211> 38
<212> DNA
<213> Artificial sequence

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<220>
<223> Description of the artificial sequence:PCR Primer

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<400> 63
cggaacgagg gcaggtgaag atgatgtcgg tgggtgccg 38

<210> 64
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<212> DNA
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<221> CDS
<222> (1)..(1266)
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Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
20 25 30

gga aat gat gtc gtg gtt gtc tgc tcc gca atg gga gac acc acg gat 144
Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
35 40 45

gaa ctt cta gaa ctt gca gcg gca gtg aat ccc gtt ccg cca gct cgt 192
Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg
50 55 60

gaa atg gat atg ctc ctg act gct ggt gag cgt att tct aac gct ctc 240
Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
65 70 75 80

gtc gcc atg gct att gag tcc ctt ggc gca gaa gcc caa tct ttc acg 288
Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
85 90 95

ggc tct cag gct ggt gtg ctc acc acc gag cgc cac gga aac gca cgc 336
Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
100 105 110

att gtt gat gtc act cca ggt cgt gtg cgt gaa gca ctc gat gag ggc 384
Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
115 120 125

aag atc tgc att gtt gct ggt ttc cag ggt gtt aat aaa gaa acc cgc 432
Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
130 135 140

gat gtc acc acg ttg ggt cgt ggt ggt tct gac acc act gca gtt gcg 480
Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala
145 150 155 160

ttg gca gct gct ttg aac gct gat gtg tgt gag att tac tcg gac gtt 528
Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
165 170 175

gac ggt gtg tat acc gct gac ccg cgc atc gtt cct aat gca cag aag 576
Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
180 185 190

ctg gaa aag ctc agc ttc gaa gaa atg ctg gaa ctt gct gct gtt ggc 624
Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
195 200 205

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 <212> PRT
 <213> LysC mutant

<400> 65

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 Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
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 Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
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 Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
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 Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
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 245 250 255
 Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
 260 265 270
 Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
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Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
290 295 300

Asp Gly Thr Thr Asp Ile Ile Phe Thr Cys Pro Arg Ser Asp Gly Arg
305 310 315 320

Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr
325 330 335

Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
340 345 350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
355 360 365

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
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Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr
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Ala Gly Thr Gly Arg
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<210> 66
<211> 5860
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: plasmid

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<210> 67
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<212> DNA
<213> Artificial sequence

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```

<220>
<223> Description of the artificial sequence:PCR primer

```

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<400> 67
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<210> 68
<211> 34
<212> DNA
<213> Artificial sequence

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<220>
<223> Description of the artificial sequence:PCR primer

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<400> 68
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<210> 69
 <211> 6472
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: plasmid

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